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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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Sequence 12, Appl
Sequence 12, Appl
Sequence 17, Appl
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sequence 4, Appii	Sequence 4, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 20, Appl	Sequence 24, Appl	•	•	Sequence 20, Appl	Sequence 24, Appl	Patent No. 5217867	Sequence 2, Appli	Sequence 19, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 18, Appl	Patent No. 5223606	Sequence 2, Appli

ALIGNMENTS

US-08-764-870-15 Patent No. GENERAL I Sequence 15, APPLICATION NUMBER: US 60/008,543 FILING DATE: 13-DEC-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/008,606 FILING DATE: 14-DEC-1995 ATTORNEY,ACENT INFORMATION: NAME: NAKAMURA, Jackie N REGISTRATION NUMBER: 35,966 REFERENCE/DOCKET NUMBER: UCAL-246/0: TELECOMMUNICATION INFORMATION: TELEPHONE: (650)843-5000 INFORMATION FOR SEQ ID NO: 1 APPLICANT: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60 FILING DATE: 13-DEC-1995 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICANT: NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: CURRENT APPLICATION DATA: TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand TITLE OF INVENTION: Binding Domains APPLICANT: APPLICANT: APPLICATION NUMBER: US/08/764,870 FILING DATE: 13-DEC-1996 CLASSIFICATION: 530 STREET: Five Pa CITY: Palo Alto STATE: CA LENGTH: COUNTRY: ADDRESSEE: INFORMATION: 94306 6236946 Application US/08764870 E: Cooley Godward Five Palo Alto Square, 984 amino acids USA West, Brian Kushner, Peter J Apriletti, James W Fletterick, Robert Wagner, Richard L Scanlan, Thomas S Baxter, John D us 60/008,540 16 15: UCAL-246/01US 3000 El Camino

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Sequence 15, Application US/08980115 patent No. 6266622 GENERAL INFORMATION: APPLICANT: Scanlan, Thomas S.
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TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND FILE REFERENCE: UCAL-246/02US
CURRENT FILING DATE: 1997-11-26
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: U8/06/980,115
CURRENT FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
INDICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
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UNIMER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 15
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FEATURE:
NAME/KEY: DOMAIN
LOCATION: (695)..(969)
OTHER INFORMATION: minimal ligand binding
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APPLICANT: Fletterick, Robert
APPLICANT: Wegner, Richard L.
APPLICANT: Wushner, Peter J.
APPLICANT: Apriletti, James W
APPLICANT: West, Brian L.
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                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/ACENT INFORMATION:
NAME: NAKAMULTA, Jackie N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
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                                                                                           REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nuclear Recepto TITLE OF INVENTION: Binding Domains NUMBER OF SEQUENCES: 16
                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Five Pal
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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              STRANDEDNESS:
TOPOLOGY: 15
                                                                                                                                   NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,9
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                     LENGTH:
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Apriletti, James W
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Fletterick, Robert
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               linear
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APPLICANT: Scanlan, Thomas S.

APPLICANT: Baxter, John D.

APPLICANT: Fletterick, Robert J.

APPLICANT: Wagner, Richard L.

APPLICANT: Washner, Peter J.

APPLICANT: Apriletti, James W.

APPLICANT: West, Brian L.

APPLICANT: Shiau, Andrew K.

TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIG
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Best Local Similarity
Matches 239; Conserv
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                          Patent No. 6266622
CURRENT APPLICATION NUMBER: US/08/980,115 CURRENT FILING DATE: 1997-11-26
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EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: DOMAIN
; LOCATION: (506)..(762)
; OTHER INFORMATION: minimal ligand
US-08-980-115-13
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Best Local Similarity
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                  WRSYKHTNSQFLYFAPDLVFNE 837
                                                                                                                            PPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYD 755
TGVSQETSENPGNKTIVPATLPQ-------LTPTLVSLLEVIEPEVLYAGYD 549
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                                                                                    SSKPDTAENLLSTLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALS 815
                                                                                                                                                                                                                NYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPP 695
                                                                                                                                                                                                                                                               SSPSMRPDVSSPPSSSSTATTGPPPKLCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQH
                                                                                                                                                                                                                                                                               SSTIR-----SVSTGSS-RPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQH
 WRSYRQSSANLLCFAPDLIINE
                                                               SSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALG
                                                                                                                                                                                                 NYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKGI-----
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 631
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RESULT 5
US-07-716-827C-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTIN Release #1
CURRENT APPLICATION DATA:
CAPPLICATION UMBER: US/07/716
FILING DATE: 19910619
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: WTS/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chakraborti, P. K.
APPLICANT: Garabedian, M. J.
TITLE OF INVENTION: SUPER GLUCOCORTICOID RECEPTORS
NUMBER OF SEQUENCES: 5
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MEDIUM TYPE: Floppy disk
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APPLICANT: Yamamoto, K. R
APPLICANT: Chakraborti, P
APPLICANT: Garabedian, M.
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LENGTH: 795 amino acids
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OPERATING SYSTEM:
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VVPSPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKI 417
                                                                  NINNSRCSVSSP----SNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRD 357
                                                                                                  QNRKSQT-----GTNGGSVKLYPTDQSTFDLLK-DLEFSAGSPSKDTNESPWRSDLLIDE
                                                                                                                                    ENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSVSSPA
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                                                                                                                                                                                                                                                                       ONOOGSMSPAKIYONVEOLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAIV 181
                                                                                                                                                                                                                                                                                                         QQQQQQQQQQQQQQQPG------LSKAVSLSMGLYMGETETKVMGNDLGYPQ 127
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o. 5215916
                                     NLLSPLAGEDDPFLLEGNTNED-
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20036-5601
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X: (202)822-8944
6714627 CUSH
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RESULT 6
US-08-764-870-14
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      APPLICATION NUMBER: US 60/UU0, JTU
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
US 60/008,543
                                                                                                                                 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nuclear Receptor
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: West, Brian
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                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 STREET: Five Pal
CITY: Palo Alto
                                                                                     APPLICATION NUMBER: US/08/764,870 FILING DATE: 13-DEC-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                                        COUNTRY:
APPLICATION NUMBER: FILING DATE: 13-DE
                                                                                                                                                                                                                                                         STATE:
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Baxter, John D
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13-DEC-1995
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Best Local Similarity
Matches 253; Conserv
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APPLICATION NUMBER: US 60/
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                         613
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TOPOLOGY: li
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                                                                                                                                                     LRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIID 648
                                                                                                                                                                                                                                                                                         LECILYKAEGAPPQQGPFAPPPCKAPGASGCLLPRDGLPSTSASAAAAGAAPALYPALGL
                                                                                                                                                                                                                                                                                                                                                                                                                                           AFAPPRTSPCASSTPVAVGDFPDCAYPPDAEPKDDAYPLYSDFQPPALKIKEEEEGAEAS 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EN-----RGSRSHSPAHASNVGSPLSSP-----LSSMKSSISSPPSHCSVKSPV 285
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               TTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLS
                                                                                                                                                                                                                                                 QGTISLSRSARDQSFQHLSSFPPVNTLYESWKSHGDLSSRRSDGYPVLEYI-PENVSSST 588
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                                                         KIRRKNCPACRLRKCCQAGMVLGGRKFKKFNKVRVVRALDAVALPQPLGVPNESQALSQR 672
                                                                                           KIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHE-EQPQQQQPPPPPPPPPQSPEEG
                                                                                                                                 PQ--YSFESLPQKICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVD
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; pred. No. 4.8e-51;
95; Mismatches 221;
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-----PYLNYLRPDSEASQS
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; NAME/KEY: DOMAIN
; LOCATION: (659)..(918)
; OTHER INFORMATION: minimal ligand binding
US-08-980-115-14
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CURRENT APPLICATION NUMBER: US/08/980/115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
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APPLICANT: Baxter, John D.
APPLICANT: Fletterick, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
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10, 6266622
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Best Local
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EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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                                                                                                      VNNAFSYTASGTSAGSSTLRDVVP---SPDTQ-----EKGAQEVPFP-----KTE 378
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 EEDSSESEESAGPL-----LKGKPRALGGAAAGGGAAACPPGAAAGGVALVPKEDSRFSA
                                                                     LMSR-SGCKVGDSSGTAAAHKVLPRGLSPARQLLLPASESPHWSGAPVKPSPQAAAVEVE
                                                                                                                                           SGPG----QSQPSPPA-----CEVTSSWCLFGPELPED-----PPAAPATQRVLSP
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                                  EVESAISNGVTGQLNIVQYIKPEP-----DGAFSSSC-----LGGNSKI-NSDSSFSV 425
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Pred. No. 4.8e-51;
5; Mismatches 221
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TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA, NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
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Best Local Similarity
                                                                                                                                                                                   Matches 138;
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                          LENGTH: 363
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FILING DATE: 17-DEC-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLNRLAGKOMIQYVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSOFL 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIRRKNCPACRLRKCCQAGMYLGGRKFKKFNKVRVVRALDAVALPQPLGVPNESQALSQR 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P----IKQES----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLS 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIRRKNCPACRLOKCLQAGMNLGARKSKKLGKLKGIHE-EQPQQQQPPPPPPPPPQSPEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFAPPRTSPCASSTPVAVGDFPDCAYPPDAEPKDDAYPLYSDFQPPALKIKEEEEGAEAS
                         LVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVK 782
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                                                           CCQAGMVLGGRKFKKFNKVR-VMRALDAVALPAPVGIPNES--QRITF----SPSQEIQ
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                                                                                                                                                                                   Conservative
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                                                                                                                                                                                   16.6%; Score 732.5; DB 6 57.0%; Pred. No. 1.4e-46; ative 37; Mismatches 46
 --INLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVK
                                                                                                                                                                                                                                                                                                                                          US/07/134,130
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                                                                                                                                                                                       Indels
                                                                                                                                                                                                                  Length
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; LENGTH: 918 a
; TYPE: amino a
; TOPOLOGY: lin
; MOLECULE TYPE:
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US-09-041-886-11
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TTTLE OF INVENTION: Polypeptides and Methods of Use
TTTLE OF INVENTION: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09041886 Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                             Ouery Match 16.4%; Score 726; DB 4; Length 918; Best Local Similarity 29.5%; Pred. No. 1.7e-45; Matches 229; Conservative 79; Mismatches 197; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
   452
                                                                               415
                                                                                                                 178
                                                                                                                                                                                                                                                                                                       238 SPNAENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSV 297
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                                                                                                                                                                                                                          298 SSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRD 357
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---FMDGSYFSFMDDKDYYSLSGILGPPVPGFDG---NCEGS--
                                     STISDNAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVRPTPCAPLAE 283
                                                                                                                 ILSEASTMQLLQQQ----QQEAVSEGSSSGRA------REASGAPTSSKDNYLGGT 223
                                                                                                                                                                                                                                                                  SPQAHRRGPTGYL-----VLDEEQQP-SQPQSALECHPERGCVPEP-----GAAVAASK 137
                                                                           SKINSDS-----SFSVPIKQESTKHSCSGTSFKGN------PTVNPFP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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 487
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	WAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE 837 : :	783 1	P &
		108	Db
	VPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVK 782	723	Qy
	CLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPQSPEEGTTYIAPAKEPSVNTA 722	61 (Qy db
	CLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQK 662	1 1	Qy Db
4	ry Match 16.1%; Score 713.5; DB 6; Length 356; t Local Similarity 60.0%; Pred. No. 3.6e-45; ches 141; Conservative 24; Mismatches 45; Indels 25; Gaps	Query Ma Best Loca Matches	
	NG DATE: 17-DEC-1987 APPLICATION DATA: 7: TH: 356	SEQ ID NO:7: LENGTH: 223606-7	5 · · · · · · · · · · · · · · · · · · ·
	NTION: STEROID/THYROID IATELY EXPRESSED IN HUUENCES: 11 CATION DATA:	TITLE ROTEIN II NUMBE	,, ,, ,, ,, ,, ,, ,, ,, ,, ,, ,, ,, ,,
	5223606 ANT: BLAUDIN DE THE, HUGHES;MARCHIO, AGNES;TIOLLAIS, EAN, ANNE	RESULT 10 5223606-7 ;Patent No. 522360 ; APPLICANT: B ;PIERRE;DEJEAN, AN	RE. 52 ; P.
	: :: : : : : : :	15	Db *
	QKLTVSHIBGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHV 714 KWAKVLPGFKNLPLEDOITLIOYSWMCLSSFALSWRSYKHTNSOFLYFAPDLVFNE 837	781 ·	Ov Db
	00	25	Qy
	AGMTLGARKLKKLGNLK-LQEEGEASSTTSPTEETT 655	620 E	Db
	AGMNIGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPPPPPPSPEGTTYIAPAKEPSVNTALV 724	665 Q	у
	:	560	ρb
	CGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCL 664	605	γQ
	CVKSEMGPWNDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCL 559	517	Db
	ENVSSSTLRSVSTGSSRPSKI	556	Qy
	GGGGGGGGEAEAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSPT 516	462	DЪ
	SLSR	515 -	Qy
	GDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPCGGGGGGGGGGGGGGGGG 461	402 Y	Db
		504 -	Qy
	: :	342 Y	Db
		488 -	Qy
	CKGSLLDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLELPSTLSL 341	284 (DЪ

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RESULT 11
US-08-764-870-16
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Best Local Similarity
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APPLICANT: Scanla
APPLICANT: Baxter
                                                                                                                                                                                                            Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION UNIMBER: US 60/008,543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand TITLE OF INVENTION: Binding Domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 6 FILING DATE: 13-DEC-1995
 150
                    661 QKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVN 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                 RKCYEAGMTLGARKLKKLGNLK-LQEEGEASS-----TTSPTEETT----
                                                                                                                                           PSPTCVKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYYFP----
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                                                                                                                                                                                                                                                                                                                                                                                        452 amino acids
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                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                            15.5%; score 686.5; DB 4;
48.2%; pred. No. 5.2e-43;
htive 33; Mismatches 66;
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                                                                                                                                                                                                                                               Length 452;
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; LOCATION: (184)...(437)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                 Matches 145;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
CURRENT FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/008,606 EARLIER FILING DATE: 1995-12-14 EARLIER APPLICATION NUMBER: 60/008,543 EARLIER FILING DATE: 1995-12-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/764,870 EARLIER FILING DATE: 1996-12-13
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NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: West, Brian L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Local Similarity 48.2%;
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MIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFN 836
                                                                    TALVPOLSTISR----ALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKO
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                                                ----QKLTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQ
                                                                                                                       RKCYEAGMTLGARKLKKLGNLK-LQEEGEASS----
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o. 6266622
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                                                                                                                                                                                                                                                                                                                                                 Score 686.5; DB 4
Pred. No. 5.2e-43;
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                                                                                                                      Query Match
Best Local Similarity
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Patent No. 623694
GENERAL INFORMAT
                                                                                                           Matches
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                             NAME: NAKAMUTA, JACKIE N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIDI TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                 553 VNTLVES-----
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Wagner, Richard L
                                                                                                           Conservative
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-WKSHGD----LSSRRSDGYPVLE-----YIPEN-----
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                                                                                                        Score 445.5; DB 4;
Pred. No. 6.1e-25;
B; Mismatches 120;
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: LOCATION: (287)..(549)
: OTHER INFORMATION: minimal ligand binding
US-08-980-115-12
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                                                                                                                                          Query Match
Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 12
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SOFTWARE: PatentIn Ve
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                                                                                                                                                                                                                                                                                                                    LENGTH: 595
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     FEATURE:
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                                   553 VNTLVES---
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100 LNSVSPSPLMILHPPPQLSPFLQPHGQQVPYYLENEPSGYTVREAGPPAFYRPNSDNRRQ 159
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                                                                     PEGAAYEFNAAAAANAQVYGQTGLPYGPGSEAAAFGSNG
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FILING DATE: 1997-11-26
APPLICATION NUMBER: 08/764,870
FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/008,540
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Pred. No. 6.1e-25;
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US-08-836-520A-17
; Sequence 17, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
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US-08-836-620A-17
                                                                                                                              Matches
                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
DRIGITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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 100
                              553 VNTLVES------WKSHGD----LSSRRSDGYPVLE-----YIPEN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 08-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 9605550.4 FILING DATE: 15-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLP 794
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LNSVSPSPIMILHPPPQLSPFLQPHGQQVPYYLENEPSGYTVREAGPPAFYRPNSDNRRQ 159
                                                                                                                              al Similarity 28.7
                                                               PEGAAYEFNAAAAANAQVYGQTGLPYGPGSEAAAFGSNG
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                                                                                                                           Score 442.5; DB 2;
Pred. No. 1e-24;
Prematches 120;
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                                                                                                                                                               Length 591;
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                                LEDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNELLARVREG
                                                                                                                                    -----RDDGEGRGEVGSAGD--------MRAANLWPSPLMIKRSKKNSLALSLT 311
                                                                                                                                                                   PPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISRA--LTPSPVMV-------
                                                                                                                                                                                                   MCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLK-HKRQ------
LHDQVHLLECAWLEILMIGLVWRSMEHPVK--LLFAPNLLLDRNQGKCVEG
                                                                  ADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLT
                                                                                  -----LENIEPETVYAGYDSSKPDTAENLLSTLNRLAGKOMIQVVKWAKVLPGFKNLP 794
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Search completed: September 13, 2002, 10:16:25 Job time: 29 sec

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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
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Listing first 45 summaries
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587.027 Million cell updates/sec
Ligand binding dom
Sequence of the hu
Sequence of the pr
Mutant nuclear glu
Ligand binding dom
Green fluorescent
Human progesterone
Ligand binding dom
Rat androgen recep
Rat androgen recep
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17 AAR90714			AAB6064											~				22 AAG84512				22 AAG84507										21 AAY78914	18 AAW14783
DNA-binding domain	Murine mER beta-1	Human oestrogen re	Human oestrogen re	Human Oestrogen re	Human estrogen rec	Human oestrogen re	Human oestrogen re	Rat oestrogen rece	Protein encoded by	Rat rER beta-4 clo	Protein encoded by	Ħ	Human estrogen rec	Human oestrogen re	0	Ligand binding dom	_	Ligand binding dom	Human androgen rec	Androgen receptor.													

ALIGNMENTS

RESULT ...
AAY2162
AAY217
AC AAY2
AC Thyr
KW alpri
KW plas
KW plas
KW plas
COS Home
COS Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glcerophosphate dehydrogenase; cardiac; obesity; triglyceride; plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor. Ligand binding domain of nuclear receptor hMR. 11-AUG-1999 (first entry) AAY21622; AAY21622 standard; 03-JUN-1999 W09926966-A2 Homo sapiens 26-NOV-1997; 25-NOV-1998; 97US-0980115 98WO-US25296 protein; 984 ₽

Modulating activity of a thyroid hormone receptor

WPI; 1999-357810/30

Apriletti JW, Scanlan TS,

), Baxter JD, Fletterick RJ, K Shiau AK, Wagner RL, West BL;

Kushner

(REGC) UNIV CALIFORNIA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA encoding hormone recpetors comprising glucocorticoid, mineralocorticoid, and novel hormone receptors
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                    Recombinant DNA encoding hormone recpetors - comprising glucocorticoid, mineralocorticoid, and novel hormone receptors
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                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of a mutant nuclear glucocorticoid CC receptor (NGR), especially mutated in the region encoding the ligand CC binding domain (LBD), such that the activity of the receptor is induced CC more strongly by a synthetic glucocorticoid ligand than by a natural CC glucocorticoid ligand. The mutation is a point mutation in the coding Sequence (a translition mutation) generated by site-directed mutagenesis. This causes a replacement of the Ile residue at position 747 with a Thr CC This causes a replacement of the Ile residue at position 747 with a Thr CC The mutant coding sequence is used to generate a fusion protein CC comprising a protein whose activity is to be regulated by and fused to the NGR sequence. The protein is preferably a recombinase, especially the Cre recombinase from bacteriophage P1 (see AAV05702). The sequence cencoding the fusion protein, and vectors containing it, are used to treat cells either ex vivo or in vitro for use in gene therapy. Vectors containing and expressing the protein allow the transfer of heterologous genes to the cells genome by recombinase-directed recombination at loxp sites. By using a mutated LBD, normal physiological levels of the cligand will not induce recombination. This requires an increased level of
                                                                                                                                                                                                                              Query Match
Best Local Similarity
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ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicolas
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lleesianlnrstsvpenpkssastavsaaptekefpkthsdvsseqqhlkgq---
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                                                                 {\tt llvdfpkgsvsnaqqpdlskavslsmglymgetetkvmgndlgfpqqgqislssgetdlk}
                                                                                                     CSVSSPSNTNNRS---TLSSPAASTVG-----SICSPVNNAFSYTASG---TSAGSSTLR 356
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                                  -PDTQEKGAQ-----EVPFPKTEEVESAISNGVTGQLNIVQYI
                                                                                                                                                                                                                              19.4%; Score 856; DB 18; 35.0%; Pred. No. 3.4e-45;
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                                                                                                                                                                                                                                                                                                            Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glcerophosphate dehydrogenase; cardiac; obesity; triglyceride; plasma cholestero!, anti-hypertriglyceridaemic; atherosclerosis; GPD thyroid hormone replacement therapy; nuclear receptor.
                                         Modulating activity of a thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1999
                                                                                                              Apriletti JW,
                                                                                                                                        (REGC ) UNIV CALIFORNIA
                                                                                                                                                                       26-NOV-1997;
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Disclosure; Fig 3A-R; 447pp; English

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Best Local Similarity 35.0
Matches 239; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasma cholesterol and triglyceride levels and can be used as anti-
hypertriglyceridaemic agents. The compound may also be used for treating
atherosclerosis and may be indicated in thyroid hormone replacement
therapy in patients with compromised cardiac function. Sequences
AAY21621- 636 amino acid sequences of ligand binding domains of several
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPEPDGAFSSSCLGGNSKI--NSDSSFSV-----PIKQESTKHSCSGTSFKGNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVVPS-----PDTQEKGAQ------EVPFPKTEEVESAISNGVTGQLNIVQYI 398
                                                                                                                                                                                            SSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALS 815
                                                                                                                                                                                                                                                                                                                                                                       sspsmrpdvssppsssstattgpppklclvcsdeasgchygvltcgsckvffkravegqh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 856; DB 20; 35.0%; Pred. No. 3.4e-45; tive 83; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SFMDDKDYY--SLSGILGPPVPGFDGNCE
                                                                                                                                                                                                                             -----ltptlvslleviepevlyagyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                 -qqat
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AAW17789 standard; Protein; 1070

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122 QNQQGSMSPAKIYQNVEQLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAIV

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                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                 Matches 261;
                                                                                                                                                                                                                         site in chromatin using the fluorescently-labelled GR. This provides the direct opportunity to visualise receptor/target interactions and can be used to screen for ligands that activate gene targetting or translocation of steroid receptors in the nucleus of a mammalian cell.
                                                                                                                                                                                                                                                                                          A fusion protein (AAW17789) comprises jellyfish green fluorescent protein (GFP) fused to rat glucocorticoid receptor (GR) via a Gly-Ala repeat linker. The GFP moiety contains an S65T substn. and the GR has a C656S substn. that humanises the protein and increases binding affinity for its ligand. Cell line 3134 (APCC CRL-119988), contg. a number of steroid receptor response elements in array, is used to visualise directly the interaction of GR and its binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green fluorescent protein; GFP; steroid receptor; transcription
                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                               elements - can be directi
labelled steroid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian cell having a plurality of steroid receptor response elements - can be directly detected when bound by fluorescently
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT68656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                              306
                                                                                                       6 YHSLPEGLDMERRWGQVSQAVERSSLGPTERTDENNYMETVNVSCVSGAIPNNSTQGSSK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1997-319778/29
                       EKQELLPCLQQDNNRPGILTSDIKTELESKELSATVAESMGLYM----DSVRDADYSYEQ
                                                                            ykslrgg-----atvkvsasspsvaaasqadskqqrilldfs--kgstsnvqqrqqqq 356
                                                                                                                                                                                                                                                                                                                                                                                                      9; Page 67-72; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fluorescent
                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
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                                                                                                                                                                                                   1070 AA;
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "glucocorticoid receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= GFR
/note= "green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gs
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                                                                                                                                              19.1%;
30.1%;
                                                                                                                                88;
                                                                                                                              Score 845.5; 1
Pred. No. 2.4e
88; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluorescent protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucocorticoid receptor;
factor; DNA binding mole
                         -lskavslsmglymgetetkvmgndlgypg
                                                                                                                                               .4e-44;
                                                                                                                                                          DB 18;
                                                                                                                                                      .Length 1070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tusion
                                                                                                                                 Indels
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181
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RESULT
AAY97297
ID AAY9
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     24 - AUG - 2000
                                                           WO200049147-A1
                                                                                                              Homo sapiens.
                                                                                                                                                                                                                          regulation; breast cancer; ovarian cancer;
                                                                                                                                                                                                                                                Recombinant DNA; gene therapy; hormone responsive element; transgene; HRE; haemophilia; clotting factor IX; vaccine;
                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY97297;
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                                                                                                                                                                                                                                                                                                                                   progesterone
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                                                                                                                                                                                                                                                                                                                                   receptor B-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 AA
                                                                                                                                                                                             fibrosis; hormone; receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        inappropriate responses to hormones, for example hormone dependent cancers such as breast, ovarian, and endometrial cancers and prostate cancer. The transgene may also be used to replace a defective gene resulting in such genetic disorders as haemophilia, von Willebrand disease, and cystic fibrosis. Vectors comprising these constructs where the transgene is human clotting factor IX can be used for treating blood clotting disorders such as haemophilia A or B on administration to an organism or to a cellular system. The constructs have applications in gene therapy for treating haemophilia when the transgene encodes a clotting factor such as clotting factor IX. The advantage of this system is that the hormone-hormone receptor complex contains a hormone receptor that becomes activated after binding of its specific hormone. The hormone receptor in the activated state is able to recognise and bind to its specific hormone responsive
                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                        nucleic acid carrying a transgene encourages binding of a hormone-hormone receptor complex. Thus the activated hormoacts as a link between the nucleic acid carrying the transhormone known to interact with the cell membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The constructs can be used to up-regulate or down-regulate target genes and for the delivery of vaccines. The constructs preferably comprise a transgene which encodes a protein which is lacking in variety of genetic disorders or involved in conditions related in variety of genetic disorders or involved in conditions related in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid constructs are described which comprise an hormone responsive element (HRE) and a transgene (T). Alternatively the nucleic acid construct, comprises at least one HRE and a transgene, where one of the HREs is not functionally linked to the transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 92-95; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid construct useful in gene therapy comprising hormone responsive element and transgene in which the hormone responsive element is not functionally linked to the transgene
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                                                                                                                                                                   SPSVCSPLNMTSSVCSPAG----INSVSSTTASFGSFPVHSPITQGT--PLTC---SPNA 241
  SSPNNVTLRSSVSSPANINNSRCSVSS------PSNTNNRSTLSSPAASTVGSICSP 336
                                       ektqdqqslsdvegaysraeatrgaggssssppekdsglldsvldtllap-----
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                                                                                                                                                                                                            Score 806; DB 21;
Pred. No. 5.8e-42;
5; Mismatches 231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glcerophosphate dehydrogenase; cardiac; obesity; triglyceride; plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor.
       WPI; 1999-357810/30
                                                                         Apriletti JW,
Scanlan TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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The invention relates to a method for modulating activity of a thyroid hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-glcerophosphate dehydrogenase (GPDH) levels, at levels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lower total plasma cholesterol and triglyceride levels and can be used as anti-hypertriglyceridement. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences expressed that the compound also be used as a compound and the compound also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences
Sequence
                                                        members of the nuclear receptor superfamily.
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  933
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  ΑA;
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Ъ 밁 Qy DЬ Вb Qy В D 밁 2 613 649 518 482 466 338 444 278 426 223 379 164 337 242 191 122 286 72 20 $\verb|kirrkncpacrlrkccqagmvlggrkfkkfnkvrvvraldavalpqplgvpnesqalsqr|$ EVESAISNGVTGQLNIVQYIKPEP------DGAFSSSC-----LGGNSKI-NSDSSFSV spevgspl-----lcrpaagpfpgsqtsdtlpevsaipis---ldgllfprpcqgqdpsd 71 SPSVCSPLNMTSSVCSPAG----INSVSSTTASFGSFPVHSPITQGT--PLTC---SPNA KIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHE-EQPQQQQPPPPPPPPPPQSPEEG LRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIID nglpqlgyqaavlk----eglpqvyp-----QGTISLSRSARDQSFQHLSSFPPVNTLVESWKSHGDLSSRRSDGYPVLEYI-PENVSSST lecilykaegappqqgpfapppckapgasgcllprdglpstsasaaaagaapalypalgl $ars prsylvagan paaf pdf pl q pp pp l pp rat ps r p geaav taa pasas vs sass s \mathfrak{gst}$ ----YYSLSGI---a fapprt speass tpv avgd fpd cayppd aepkd dayplysd fqppalkike eee gae as-----NPTVNPFP----FMDGSYFSFMDDKD--- ${\tt prvalveq} dap {\tt mapgrsplattvm} dfih {\tt vpilpln} hall {\tt aartrqlle} desydga {\tt gaas}$ P----IKQES----eedsseseesagpl-----lkgkpralggaaagggaaacppgaaaggvalvpkedsrfsa lmsr-sgckvgdssgtaaahkvlprglsparqlllpasesphwsgapvkpspqaaaveve VNNAFSYTASGTSAGSSTLRDVVP---SPDTQ-----EKGAQEVPFP-----KTE sgpg----qsqpsppa-----cevtsswclfgpelped-----ppaapatqrvlsp SSPNNVTLRSSVSSPANINNSRCSVSS-----PSNTNNRSTLSSPAASTVGSICSP 336 ektqdqqslsdvegaysraeatrgaggssssppekdsglldsvldtllap------EN-----RGSRSHSPAHASNVGSPLSSP-----LSSMKSSISSPPSHCSVKSPV 285 EGSGFPVGIKQEPDDGSYYPEASIPSSAIVGVNSGGQSFHY-RIGA ---LGPPVP-------TKHSCSGTSFKG----------pylnylrpdseasqs -GFD 457 425 163 648 588 529 397 241 672 612 554 517 481 337 443 121 707 465 277 222

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Query Match Best Local Similarity

18.1%; Score 801; DB 20; 29.5%; Pred. No. 1.2e-41;

Length Indels

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                                                                                                                                                                                                                     Androgen receptor protein (AR) is used to produce mono- or poly-clonal antibodies. These are used for the detection and quantification of AR in the presence of endogenous androgen, as androgen will not interfere with binding. They may be used in assays to determine and quantify cellular distribution of AR in tumour tissue, and are esp. useful for evaluating prostate cancers to determine responsiveness to androgen withdrawal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP93110 standard;
                                                                                                                                                                                                                                                                                                                             DNA encoding androgen receptor protein - useful for transforming eukaryotic hosts for protein expression and subsequent antibody |
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N-PSDB; AAN91773.
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                                                        VTLRSSVSSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSA
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3; Mismatches 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ISR----ALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAK
                                                                                                                                                                                                                 receptor; TR2 polypeptide;
                                                                                                                                                                                                                                        receptor DNA clone.
                                                                                                                                                                                                                                                              (first entry)
          88US-0176107
                                 89WO-US01238
                                                                                                                                                         Location/Qualifiers
                                                                                                   /product=79 kD polypeptide
                                                                                                                          /product=98
170..902
                                                                                                                                                /*tag=
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein is used to raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 3; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 QGTPLTCSPNAENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNN 290
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DB; AAN91578.
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vshiegyecqpiflnvleaiepgvvcaghdnnqpdsfaallsslnelgerqlvhvvkwak
            ISR----ALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAK 785
                                                             LGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLST
                                                                                                       ASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMN
                                                                                                                                         mgpwmenysgpygdmrldstrdhvlpidyyfp------
                                                                                                                                                        ---WKS----HGD--LSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDE
                                                                                                                                                                                     \verb|gggggssspsdagpvapygytrppqglasqegdfsasevwypggvvnrvpypspscvkse|
                                                                                                                                                                                                               GAQGTISLSRSA---
                                                                                                                                                                                                                                  enpldygsawaaaaaqcrygdlaslhggsvagpstgsppatassswhtlftaeegqlygp
                                                                                                                                                                                                                                                           ----DDGS------YYPEASIPSSAIVGVNSG------GQSFH----
                                                                                                                                                                                                                                                                                 sseagssgtleipsslslyksgavdeaaayqnrdyynfplalsgpphppppthpharikl
                                                                                                                                                                                                                                                                                                                              asllggppavrptpcaplaeckglsldegpgkgteetaeyssfkggyakglegeslgcsg
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                                                                                          asgchygaltcgsckvffkraaegkqkylcasrndctidkfrrkncpscrlrkcyeagmt 608
                                                                                                                                                                                                                                                                                                                                                      -----PTVNPFP-----FMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kD product starts at the first Met codon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              new androgen receptor and TR2 polypeptide(s) - able derived antibodies, useful for receptor assay and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%;
30.1%;
                                                                                                                                                                                                              ---RDQSFQHLSS-----FP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 758.5; DB 1; Pred. No. 5.2e-39; 83; Mismatches 208
                                                                                                                                                                                                                                                                                                        -QEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----aapstlsllgp-----tfpglss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -qqpsqqqsaseghpesgclpepgaatapg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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                                                                                                                                                                                                              -PVNTLVES-
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            156
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рь Фу Qy Qy

밁 Ş Ъ δ Вþ Š Дb δ DЬ δÃ B δÃ B Š д δõ 뫄 Qy

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Matches 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was deduced from a cDNA clone isolated by screening a rat ventral prostate lambda gtll library in E.coli Y1990. The sequence is very similar to that of human AR and in the DNA-binding domain it is identical to that of hAR DNA-binding domain. Homology comparisons with other known steroid receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Androgen receptor and TR2 DNA binding proteins - DNA sequences and antibodies for detection and quantification methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rAR; DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR12224 standard; Protein; 902 AA
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        indicate that rAR is more closely related to glucocorticoid, mineralo-corticoid and progesterone receptors than to v-erb-A or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ARCH-)
   399
                                                                                                                                                                                                                                231 QGTPLTCSPNAENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNN
                                                                                                                                                                                                                                                                       Local Similarity
nes 229; Conserv
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                                     csadikdilseagtmqllqqqqqqqqqqqqqqqqqqqqqqqqevisegsssvrar-----
                                                                                                                                                      VTLRSSVSSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSA
   KPEPDGAFSS---SCLGGNSKINSDS-----
                                                                                                                 kglpqqppappdqdds
                                                                                                                                                                                        qqhpedgspqahirgttgylaleee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Fig 3; 79pp;
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    oestrogen, vitamin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "cysteine-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                     17.0%;
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                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                     Score 753.5; DB 12
Pred. No. 1.1e-38;
5; Mismatches 225;
                                                                           QEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYI
                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                          -qqpsqqqsaseghpesgclpepgaatapg
                                                                                                                 ----aapstlsllgp-----tfpglss
   -SFSVPIKQESTKHSCSGTSFKGN----
                                                                                                                                                                                                                                                                                                           DB 12;
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 밁
           Oligonucleotide(s) antisense to human androgen receptor and acidic FGF genes - used to inhibit gene expression, for the treatment of \ensuremath{\mathsf{FGF}}
                                                                                                                                                                                                                                                      Androgen receptor; acidic fibroblast growth factor; aFGF; antisense; benign prostatic hyperplasia; prostate cancer;
                                                                                   Zamecnik
                                                                                                          (WORC-)
                                                                                                                                  20-SEP-1995;
                                                                                                                                                        20-SEP-1996;
                                                                                                                                                                                27-MAR-1997
                                                                                                                                                                                                        W09711170-A1
                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                         Androgen receptor
                                                                                                                                                                                                                                                                                                                 22-JUN-1997
                                                                                                                                                                                                                                                                                                                                         AAW14783;
                                                                                                                                                                                                                                                                                                                                                                 AAW14783 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326
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                                               1997-202879/18.
DB; AAT63407.
                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 22-28; 51pp; English
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{\tt gfrn1hvddqmaviqyswmg1mvfamgwrsftnvnsrmlyfapd1vfne}
                                                                                                                                                         RKSKKLGKLKGIHEEQPQQQQPPPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISR 732
                                                                                                                                                                                                          CHYGYVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGA
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                GFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE
                                                                                                                                                                                        \verb|chygaltcgsckvffkraaegkqkylcasrndctidkfrrkncpscrlrkcyeagmtlga|\\
                                                                                                                                                                                                                                                                                                                  \verb|ggggggeagavapygytrppqglaggesdftapdvwypggmvsrvpypsptcvksemgp|
                                                                                                                                                                                                                                                                                                                                                   -----RIGAQGTISLSRSARDQSFQH-----
                                                              iegyecqpiflnvleaiepgvvcaghdnnqpdsfaallsslnelgerqlvhvvkwakalp
                                                                                                                             rklkklgnlk-lqeegeass-----ttspteett---
                                                                                                                                                                                                                                                                                    WKS----HGD--LSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASG
                                                                                            ---ALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLP
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Pred. No. 2.6e
76; Mismatches
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                                                                                                                                                                                                                                                                                                                        This sequence represents the human androgen receptor (AR) amino acid sequence. The invention relates to a fragment of the AR corresponding to a mino acids 234-391 (see AAY78913). The fragment mediates amino acids 234-391 (see AAY78913). The fragment mediates are receptor acts as a transcription factor, regulating the expression of certain androgen responsive genes. Interaction of the AR with the protein kinase and rogen responsive genes. Interaction of the AR with the protein kinase and signal transduction pathway involves interaction with the androgen and signal transduction pathway involves interaction with the androgen according independent activation of the AR fragment and peptides derived from it can be used as agents for inhibiting androgen independent activation of the AR compounds which affect androgen independent activation of the AR. The peptides, when used in combination with androgen deprivation, and as a tool for screening confectively limit androgen mediated disease progression. These diseases and prostatic hyperplasia, hirusutism, androgenic concert. The peptides and nucleic acids encoding them, are especially used for the treatment of androgen mediated disease, and especially used for the treatment of androgen mediated disease.
                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.9
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Androgen receptor; AR; androgen-independent activation; inhibitor; cancer; benign prostatic hyperplasia; hirusutism; androgenic alopecia; acne; breast cancer; Kennedy disease; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                      cancer. The peptides and nucleic acids encoding them, for the treatment of androgen-mediated diseases, espectumours in patients deprived of androgen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening compounds and such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel non-androgen ligand binding peptides for inhibiting androgen-independent activation of androgen receptor, used screening compounds and for treatment of androgen-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1999;
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ilseastmqllqqq----qqeavsegsssgra--
                                      VVPSPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSS----CLGGN 414
                                                                                                SSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRD 357
                                                                                                                                                  spqahrrgptgyl-----vldeeqqp-sqpqsalechpergcvpep----gaavaask 141
                                                                                                                                                                                       SPNAENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSV 297
                                                                           glpqql-----pappdedd----saapstl-sllgp-
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Pred. No. 2.6e-37;
6; Mismatches 204;
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Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC; huntingtin polypeptide; Machado-Joseph disease; SCA1; SCA2; SCA6; atrophin-1; cell death; apoptosis; Huntington's disease; head trauma; Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; strok dentatorubropallidoluysian atrophy; cell proliferation; cell survival neoplastic; malignant; autoimmune; fibrotic.
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12-MAR-1998; 11-MAR-1999; 16-SEP-1999 WO9945944-A1 Homo sapiens.

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N-PSDB; AAN91772.
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ALIGNMENTS

mineralocorticoid receptor - human N;Alternate names: aldosterone receptor

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A;Map position: 4931-4931
A;Map position: 4931-4931
A;Map position: 4931-4931
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: DNA binding; transcription regulation; zinc finger F;601-880/Domain: erbA transforming protein homology <ERBA>
F;603-623/Region: zinc finger F;639-663/Region: zinc finger
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A;Title: Cloning of human mineralocorticoid receptor complementary DNA: structural A;Reference number: A29513; MUID:87263386
A;Accession: A29513
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
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A; Residues: 1-984 < ARR>
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Best Local Similarity
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ANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVVP
                                                         VKSPIMCHEKSPSVCSPLNMTSSVCSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPN
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                                                                                                                                                                                                                                                                                                                                                                 METKGYHSLPEGLDMERRWGQVSQAVERSSLGPTERTDENNYMEIVNVSCVSGAIPNNST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 4385; DB 2; ilarity 100.0%; Pred. No. 1.7e-220; Conservative 0; Mismatches 0;
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RESULT 2
A41401
mineralocorticoid receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-:
C;Accession: A41401
R;Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
Mol. Endocrinol. 3, 1877-1885, 1989
A;Title: Molecular cloning of a mineralocorticoid (type I) receptor A;Reference number: A41401; MUID:90114194
A;Accession: A41401
A;Status: preliminary
**Molecular type: mRNA
                                                                                                                                                                                                                                                       A)Cross-references: GB:M36074; NID:g205340; PIDN:AAA41583.1; PID:g205341 C;Superfamily: unassigned erbA-related proteins; erbA transforming proteins; Keywords: DNA binding; transcription regulation; zinc finger F;602-877/Domain: erbA transforming protein homology <ERBA>F;604-624/Region: zinc finger F;640-664/Region: zinc finger
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A; Residues: 1-981 <PAT>
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Best Local Similarity
Matches 746; Conserv
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              QQNQQGSMSPAKIYQNVEQLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAI
                                                       METKGYHSLPEGLDMERRWGQVSQAVERSSLGPTERTDENNYMEIVNVSCVSGAIPNNST
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QQNQQGSLSPTKIYQNMEQLYKFYKENGHRSSTLSAMSRPLRSFMPDSAASMNGGALRAI
                                                                                                                       METKGYHSLPEGLDMERRWSQVSQTLERSSLGPAERTTENNYMEIVNVSCVSGAIPNNST
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                               88.6%;
                                                                                                                                                                               ; Score 3919.5; DB 2
; Pred. No. 2.7e-196;
35; Mismatches 52;
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                                                                                                                                                                                                            Length
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Matches

Local Similarity nes 231; Conserv

Conservative

79;

Mismatches

183;

Indels 124;

Gaps

25;

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glucocorticoid receptor - guinea pig (; Species: Cavia porcellus (guinea pig) C; Date: 09-Sep-1994 #sequence_revision 09-Se C; Accession: A54273 #Sequence_revision R; Keightley, M.C.; Fuller, P.J. Mol. Endocrinol. 8, 431-439, 1994 A; Title: Unique sequences in the guinea pig A; Reference number: A54273; MUID:94329100
                                               A;Cross-references: GB:L13196
C;Superfamily: glucocorticoid recept
C;Keywords: zinc finger
E;414-668/Domain: erbA transforming
E;416-436/Region: zinc finger
E;452-476/Region: zinc finger
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A54273
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                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-771 <KEI>
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                                                                                                                                                 A; Status: preliminary
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19.6%;
                                                                                                   receptor; erbA transforming
 Score 865; DB 2; Pred. No. 1.3e-37;
                                                                          protein
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                                                                          homology
                                                                                                                                                                                        glucocorticoid
                                                                                                   protein
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A;Cross-references: EMBL:X72211
A;Cross-references: EMBL:X72211
A;Experimental source: embryonic stage 17
R;Gao, X.; Kalkhoven, E.; Peterson-Maduro, J.; van R;Gao, X.; Kalkhoven, E.; Peterson-Maduro, J.; van submitted to the EMBL Data Library, May 1993
A;Description: The expression of glucocorticoid red A;Reference number: $44047
A;Reference in S44047
A;Accession: $44047
A;Residues: 1-271,'R',273-776 <GAW>
A;Residues: 1-271,'R',273-776 <GAW>
A;Cross-references: EMBL:X72211; NID:9444042; PIDN A;Experimental source: embryonic stage 17
                                                                                                                                                                                                                                                                                                                                        glucocorticoid receptor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jan-1995 #sequence_revision 27-Oct-1995 #text_change
C:Accession: $45348; $44047; $42083
R:Gao, X.; Kalkhoven, E.; Peterson-Maduro, J.; van der Burg, B.;
Biochim. Biophys. Acta 1218, 194-198, 1994
A;Title: Expression of the glucocorticoid receptor gene is regul
A;Reference number: $45348; MUID:94289478
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
                    A; Reference number: $42083
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A; Reference number: A; Accession: S42083
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A; Residues: 1-776 <GAO>
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A;Residues: 452-501, 'p', 503, 'A', 505, 'A', 507-510, 'N', 512-518, 'M', 520-543, 'F A;Cross-references: EMBL:X77764; NID:g456373; PIDN:CAA54804.1; PID:g456374 A;Experimental source: liver C;Superfamily: glucocorticoid receptor; erbA transforming protein homology C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription: F;418-673/Domain: erbA transforming protein homology <ERBA> F;420-440/Region: zinc finger CCCC motif F;456-480/Region: zinc finger CCCC motif
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KAIPGFRNLHLDDQMTLLQYSWMFLMVFALGWRSYKQTNGSILYFAPDLVITE
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90; Mismatches
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glucocorticoid receptor, b
N;Alternate names: hGR
C;Species: Homo sapiens (m
C;Date: 04-Dec-1986 #seque
C;Accession: B93370; B3977
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A;Gene: GDB:GRL
A;Cross-references: GDB:120017; OMIM:138040
A;Cross-references: GDB:150017; OMIM:138040
A;Map position: 5q31-5q31
A;Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3
A;Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3
A;Note: the first intron occurs before the initiator codon
C;Superfamily: glucocorticoid receptor; erbA transforming protein homology
C;Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor;
E;419-674/Domain: erbA transforming protein homology <ERBA>
F;457-481/Region: zinc finger CCCC motif
E;457-481/Region: zinc finger CCCC motif
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A;Contents: annotation; domains
C;Comment: Alpha (see PIR:QRHUGA) and beta splice forms differ in their carboxyl-terminal however, it is possible that variant receptors perform tissue-specific functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; not compared with concept A;Molecule type: DNA A;Molecule type: DNA A;Residues: 385-404;441-459;480-498;573-593;621-640;665-685;718-737 A;Cross-references: GB:M60597 A;Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X03348; GB:M11050; NID:g31681; PIDN:CAA27054.1; PID:g31682 R;Encio, I.J.; Detera-Wadleigh, S.D. J. Biol. Chem. 266, 7182-7188, J. Biol. Chem. 266, 7182-7189. Piz:Catalogue of the human glucocorticoid receptor.

A;Reference number: A39779; MUID:91201378

A;Accession: B39779
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A; Residues: 1-742 < HOL>
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                       QGTISLSRSARDQSFQHLSSFPPVNTLVESW---KSHGD--LSSRRSDGYPVLEYIPENV
                                                                            KEDFIELCTPGVIKQE-KLGTVYCQASFPGANIIGNKMSAISVHGVSTSGGQMYHYDM--
                                                                                                                           GSGF----PVGIKQEPDDGSYYPEASIPSSAIVG---
                                                                                                                                                                                LSPLAGEDDSFLLEGNSNEDCKPLILPDTKPKIKDNGDLVLSSPSNVTLPQV----
                                                                                                                                                                                                                                                                                                                                KPEPDGAFSSSCLGGNSKI - - NSDSSFSV - - -
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                                                                                                                                                                                                                                                                                 -TGTNGGNVKLYTTDQSTFDILQDLEFSSGSPGKETNESPWRSDLLIDENCL
                                                                                                                                                                                                                                                                                                                                                                                                                                    --PDTQEKGAQ-----EVPFPKTEEVESAISNGVTGQLNIVQYI 398
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Pred. No. 3.7e-37;
3; Mismatches 212
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                                                             SSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALG
                                                                                          SSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALS
                                                                                                                           TGVSQETSENPGNKTIVPATLPQ-
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A;Cross-references: EMBL:X03225; GB:M10901; NID:g31679; PR;Leclerc, S.; Xie, B.; Roy, R.; Govindan, M.V. J. Biol. Chem. 266, 8711-8719, 1991
A;Title: Purification of a human glucocorticoid receptor A;Reference number: A39837; MUID:91224961 C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jul-2000
C;Accession: A93370, A39837, A39779; 156596; A03246; A32196
R;Hollenberg, S.M.; Weinberger, C.; Ong, E.S.; Cerelli, G.; Oro, A.; Lebo, I
Nature 318, 635-641, 1985 A; Reference number: A39837; A; Accession: A39837 A; Molecule type: mRNA A; Residues: 1-777 < HOL> A;Title: Primary structure and expression A;Reference number: A93370; MUID:86092206 A; Accession: A93370 N; Alternate names: glucocorticoid receptor, QRHUGA hGR alpha splice form of ı a functional human human PIDN:CAA26976.1; gene promoter-binding protei glucocorticoid PID: 931680 recept

R;Encio, I.J.; Detera-Wadleigh, S.D J. Biol. Chem. 266, 7182-7188, 1991 A;Residues: 1-394 <LEC> A;Cross-references: GB.M69104; NID:g183605; PIDN:AAA88049.1; A; Molecule type: DNA Ö PID:g553322

J. Biol. Chem. 266, 7182-7188, 1991
A;Title: The genomic structure of the human glucocorticoid receptor A;Reference number: A39779; MUID:91201378
A;Accession: A39779 not compared with conceptual translation

A; Molecule type: DNA A; Residues: 385-404;441-459;480-498;573-593;621-640;665-685;718-737 A; Status: nucleic acid sequence not shown; **SENC**

R; Weinberger, C.; Hollenbe Nature 318, 670-672, 1985 A;Cross-references: GB:M60597 A;Experimental source: placen Hollenberg, S.M.; Rosenfeld, M.G.;

A; Title: Domain structure of human glucocorticoid A; Reference number: A93373; MUID:86092211 and its relationship ç ţ

Evans,

R;Dahlman, K.; Stroemstedt, P.E.; Rae, C.; Joernval J. Biol. Chem. 264, 804-809, 1989 A;Title: High level expression in Escherichia coli A;Reference number: A32196; MUID:89093147 A; Contents: annotation; domains Joernvall,

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R;Govindan, M.V.; Pothier, F; Leclerc, S.; J. Steroid Biochem. Mol. Biol. 40, 317-323. A;Title: Human glucocorticoid receptor gene A;Reference number: 156596; MUID:92068829 A; Contents: annotation; domains engineered sequence expressed in Escherichia Palaniswami,

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A;Map position: 5q31-5q31
A;Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3
A;Introns: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3
A;Note: the first intron occurs before the initiator codon
C;Superfamily: glucocorticoid receptor; erbA transforming pr
C;Keywords: alternative splicing; DNA binding; nucleus; ster
F;419-674/Domain: erbA transforming protein homology <ERBA>
F;421-441/Region: zinc finger CCCC motif
F;457-481/Region: zinc finger CCCC motif
F;457-77/Domain: steroid binding #status predicted <STB>
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A; Residues: 1-394 <RES>
A; Cross-references: GB:S68378;
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                                                                                                                                                       SSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALG
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                                                                                                                                                                                                                                   TGVSQETSENPGNKTIVPATLPQ-
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                                                                                                                                                                                                                                                                                                            NYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKGI------QQAT 504
                                                                                                                                                                                                                                                                                                                                                                                       SSPSMRPDVSSPPSSSSTATTGPPPKLCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGTISLSRSARDQSFQHLSSFPPVNTLVESW----KSHGD--LSSRRSDGYPVLEYIPENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGF-----PVGIKQEPDDGSYYPEASIPSSAIVG-----VNSGGQSFHYRIGA 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TGTNGGNVKLYTTDQSTFDILQDLEFSSGSPGKETNESPWRSDLLIDENCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPEPDGAFSSSCLGGNSKI --NSDSSFSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PDTQEKGAQ-----EVPFPKTEEVESAISNGVTGQLNIVQYI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%;
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Pred. No. 4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SFMDDKDYY--SLSGILGPPVPGFDGNCE
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glucocorticoid receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
C;Accession: A24194; S02475; A27284; S33888; S33891
R;Mlesfeld, R.; Rusconi, S.; Godowski, P.J.; Maler, B.A.; Okret,
Cell 46, 389-399, 1986
A;Title: Genetic complementation of a glucocorticoid receptor del
A;Reference number: A24194; MUID:86272086
A;Accession: A24194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-97, 'D',99-225,'G',227-259,'D',261-344,'T',346-515 <CHA>
A;Residues: 1-97, 'D',99-225,'B;NID:956324; PIDN:CAA68545.1; PID:956325
A;Cross-references: GB:Y00489; NID:956324; PIDN:CAA68545.1; PID:956325
R;Gearing, K.L.; Gustafsson, J.A.; Okret, S.
Nucleic Acids Res. 21, 2014, 1993
A;Itle: Heterogeneity in the polyglutamine tract of the glucocorticoid receptor from A;Reference number: S33888; MUID:93261843
A;Accession: S33888; MUID:93261843
A;Accession: S33888
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A; Title: Cloning and sequence analysis of the A; Reference number: A27284; MUID:88067783
A; Accession: A27284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: DNA binding; nucleus; steroid hormone receptor;
F;75-96/Region: glutamine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d is initiated from 1-Met.
C; Superfamily: glucocorticoid receptor; erbA transforming protein homology
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                                                                                                                                                                                                                                                                                                                                                                        Вb
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A; Residues: 68-92,97,'D',99-104
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A; Residues: 68-97, 'D', 99-104
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A; Residues: 440-539 <SEV>
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A; Residues: 1-795 <MIE>
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A;Accession: S33891
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                                                                                                                                                                                                                                                                                                                                                                                                                         YHSLPEGLDMERRWGQVSQAVERSSLGPTERTDENNYMEIVNVSCVSGAIPNNSTQGSSK 65
     ENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSVSSPA 301
                                                                                                                                                                                                                                                                                                                                                                  YKSLRGG-----ATVKVSASSPSVAAASQADSKQQRILLDFS--KGSTSNVQQRQQQQ 81
                                                                                                       KSPIMCHEKSPSVCSPLNMTSSVCSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPNA
                                                                                                                                                              QGQLGLSSGETDFRLLEESI - - -
                                                                                                                                                                                                                                                                                                                 EKQELLPCLQQDNNRPGILTSDIKTELESKELSATVAESMGLYM----DSVRDADYSYEQ 121
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                                                      ANLINESTSVPE----NPKSSTSATGCATPTEKEFPK-THSDASSEQ
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30.1%;
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Pred. No. 1.4e-36;
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glucocorticoid receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 18-Nov-1994 #
C;Accession: A25691; S02212; S02214
R;Danielsen, M.; Northrop, J.P.; Ringold, G.M.
EMBO J. 5, 2513-2522, 1986
A;Title: The mouse glucocorticoid receptor: mapping
A;Reference number: A25691; MUID:87053816
A;Accession: A25691
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A; Molecule type: mRNA
A; Residues: 1-436, 'G', 438-458, 'R', 459-755 < NO2>
A; Cross-references: EMBL:X13359; NID:g51119; PIDN:CAA31739.1; PID:g51120
A; Note: neither the complete nucleic acid sequence nor the complete translation
C; Superfamily: glucocorticoid receptor; erbA transforming protein homology
                                                                                      A; Molecule type: mRNA
A; Residues: 1-436, 'G', 438-755 < NOH>
A; Cross-references: EMBL:X13358; NID:g51117; PIDN:CAA31738.1; PID:g51118
A; Note: neither the complete nucleic acid sequence nor the complete transaccession: S02214
A; Accession: S02214
                                                                                                                                                                          A;Cross references: GB:X04435; N1
R;Nohno, T.; Kasai, Y.; Saito, T.
Nucleic Acids Res. 17, 445, 198
A;Title: Novel cDNA sequence poss
A;Reference number: S02212; MUID:
A;Accession: S02212
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MUID:89098404
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C;Keywords: alternative splicing; DNA binding; nucleus; E;75-82/Region: glutamine-rich F;426-680/Domain: erbA transforming protein homology <ER F;428-448/Region: zinc finger CCCC motif F;464-888/Region: zinc finger CCCC motif F;734-783/Domain: steroid binding #status predicted <STH
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                                                     \tt MTTLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQASGN
                                                                    NANKTIVPAALPQ-
                                                                                                                           EGTTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENL
                                                                                                                                                                   IIDKIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKGIQQATAGVSQ------DTSE
                                                                                                                                                                                IIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPQSPE
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                                                                                                                                                                                                                                     SSTLRSYSTGSSRPSKICLYCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDC
                                                                                                                                                                                                                                                                           {\tt DQK-PVFNVIPPIPVGSENWNRCQGSGEDNLTSLGAMNFAGRSVFSNGYSSPGMRPD--V}
                                                                                                                                                                                                                                                                                                      DQSFQHLSSFPPVNTLVESWK----
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 LLCFAPDLIINE
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zinc finger CCCC motif
zinc finger CCCC motif
steroid binding #status predicted <STB>
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                                                                                                              LTPTLVSLLEVIEPEVLYAGYDSSVPDSAWRI
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progesterone receptor B form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996
C:Accession: I53280; B23733; A49574; A23733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Endocrinol. 7, 1603-1616, 1993
A; Title: Cloning of the rat progesterone receptor gene A; Reference number: A49574; MUID:94195318
A; Accession: A49574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 555-589,'W',591-624;742-910 <PAR2>
A;Cross-references: GB:S64044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Park-Sarge, O.K.; Mayo, K.E.
Endocrinology 134, 709-718, 1994
A;Title: Regulation of the progesterone receptor
A;Reference number: 153280; MUID:94130817
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A; Residues: 1-16 <KRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Transient expression of progesterone receptor messenger RNA in A;Reference number: A23733; MUID:92049379
A;Accession: B23733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L16922; NID:g463282; PIDN:AAA19916.1; PID:g463283
R;Park, O.K.; Mayo, K.E.
Mol. Endocrinol. 5, 967-978, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-923 < PAR1>
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les 260; Conservative
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                                   -PSAPSPPVPCGDFPDCTYPPEGDPKEDGFPVYGEFQPPGLKIKEEEEGTEAASRSPRPY
                                                                                                                                                                             KSKP-RALEGMCSGGGVTANAPGAAPGGVTLVPKEDSRFSAPRVSLEQDAPVAPGRSPLA
                                                                                                                                                                                                                  KPEPDGAFSSSCLGGNSKINS---
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-EASI--PSSAIVGVNSGGQSFH---YRI-GA-
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2.6e-35;
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A; Molecule type: mRNA
A; Residues: 1-89, 'L', 91-246, 'P', 248-281, 'Y', 283-303, 'T', 305-351, 'RLI', 355, 'S',
A; Experimental source: pituitary
C; Genetics:
A; Gene: GR
C; Superfamily: glucocorticoid receptor; erbA transforming protein homology
C; Keywords: alternative splicing; DNA binding; steroid binding; transcription:
E; 59-66/Region: glutamine-rich
E; 59-66/Region: glutamine-rich
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$60586
$corticold receptor - rainbow trout
glucocorticold receptor - rainbow trout)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997
C:Accession: $60586; $70470
C:Accession: $65586; $70470
R:Ducouret, B.; Tujague, M.; Ashraf, J.; Mouchel, N
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F;432-456/Region: zinc finger CCCC motif
F;703-752/Domain: steroid binding #status
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A;Title: Cloning of a teleost fish glucocorticoid receptor shows A;Reference number: S60586; MUID:95377204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z54210; NID:g995676; PIDN:CAA90937.1; R;Takeo, J.; Hata, J.; Segawa, C.; Toyohara, H.; Yamashita, S. FEBS Lett. 389, 244-248, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-758 < DUC>
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Matches 229; Conserv
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                                       -LSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSV----SSPANINNSRCSVSSPSNTNNR 319
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progesterone receptor form B - chicken
N;Contains: progesterone receptor form A
C;Species: Gallus gallus (chicken)
C;Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A35466; S06284; A40903; A24661; A24312; A40911; A61552
R;Jeltsch, J.M.; Turcotte, B.; Garnier, J.M.; Lerouge, T.; Krozowski, Z.; Gr
J. Biol. Chem. 265, 3967-3974, 1990
A;Title: Characterization of multiple mRNAs originating from the chicken pro
A;Reference number: A35466; MUID:90154085
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                                                       A;Title: Sequence and expression of a functional chicken A;Reference number: A40903; MUID:91042592 A;Accession: A40903
                                                                                                                    A;Cross-references: EMBL:Y00092; NID:g63744; PIDN:CAA68282.1; R;Conneely, O.M.; Dobson, A.D.W.; Tsai, M.J.; Beattie, W.G.; Mol. Endocrinol. 1, 517-525, 1987
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A; Molecule type: mRNA
A; Residues: 1-64, 'E', 65-786
                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-786 <GRO>
                                                                                                                                                                                                                          EMBO J. 6, 3985-3994, 1987
A;Title: The chicken progesterone receptor:
A;Reference number: S06284; MUID:88166640
A;Accession: S06284
                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M32732; GB:J05240; NID:g212554; PIDN:AAA49011.1; PID:g212558 R;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, M.E.; Kroembo J. 6, 3985-3994, 1987
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A; Residues: 1-786 <JEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTNSQFLYFAPDLVFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAENILISTLURLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYK 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLCTPGVIKQENDRRSFCQISSLDLPSTHNSAGSISGPSYPYGANTSTAVSLQQDQKPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKHSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYS--LSGILGPPVPGFDGNCEGSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTMDILQDLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINSDSSFSVPIKQES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLSSPAASTVGSICSPVNNAFSYTASGTS-----AGSSTLRDVVPSPDTQEKGAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPD 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRNDCIIDKIRRKNCPACRFRKCLQAGMNLEARKNKKLIRLKG------QQTTMEPNPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPAKPSGPTHKICLVCSDEASGCHYGVLTCGSCKVFFKRAVEGWRARQNTDGQHNYLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQHLSSFPPVNTLVESWKSHGDLSSRRSDGYPV----LEYIPENVSSSTLRSVSTGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- FGLYPPLPSVSDSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SRPS----KICLVCGDEASGCHYGVVTCGSCKVFFKRAVE-------GQHNYLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVGIKQEPDDGSYYPEAS--IPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNMETKPIDCSNGGNCTNVDSADQQKQLLEAGVSMPVIKTEEDADTSFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LPGSLSDLNEFYVSDEAAFLSS-LSVEDVLLED-------
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  <CON>
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                                                                                                                                                                                                                                                                   sequence,
                                                                                                                                                                                                                                                                     expression
                                                                                                      progesterone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krozowski, Z.; Gronemeyer,
                                                                                                                                            Toft,
                                                                                                                                            PID:g63745
Toft, D.O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Conneely, O.M.; Sullivan, W.P.; Toft, D.O.; Science 233, 767-770, 1986
A;Title: Molecular cloning of the chicken prog A;Reference number: A24661; MUID:86289413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: progesterone receptor; erbA transforming protein homology C;Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger F;1-786/Product: progesterone receptor form B #status predicted <MAl> F;128-786/Product: progesterone receptor form A #status predicted <MAl> F;419-682/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 136-153; 168-174; 195-228; 526-537, 'X', 539; 546-563
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein A;Residues: 128-133, 'E',135-147, 'E',149-164;546-558 <BIR>A;Residues: 128-133, 'E',135-147, 'E',149-164;546-558 <BIR>R;Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H. Mol. Cell. Endocrinol. 52, 177-184, 1987 Mol. Cell. Endocrinol. 52, 177-184, 1987 A;Title: Peptide sequencing of the chick oviduct progesterone A;Reference number: A61552; MUID:88005426 A;Accession: A61552
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A; Residues: 417-490 <252>
A; Residues: 417-490 <252>
A; Cross-references: GB:M14280; NID:g212607; PIDN:AAA49039.1; PID:g212608
A; Cross-references: GB:M14280; NID:g212608; PID:g212608; PI
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Qy
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A; Accession: A40911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 SSPAASTVGS-----ICSPVNNAFSYTASGTSAGSSTLRDVVPSPDTQEKGAQEVPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASPAAVEPGAGQDYLHVPILPLNSAF-----LASRTRQLLDVEAAYDGSAFGPRSSP--
                                                                                                                       CGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQ 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSGTSEKGNPTVNPFPFMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEGSGFPVGIKQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SVPAA----
                                                                                   CGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVDKIRRKNCPACRLRKCCQ
                                                                                                                                                                                                                                       LPQLCP
                                                                                                                                                                                                                                                                                                                                                                                                                                          EPD--DGSYYPEA---SIPSSAIV--GVNS--GGQSFHYRIGAQGTISLSRSARDQSFQH 546
   AGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVP
                                                                                                                                                                                                                                                                                                              LSSFPPVNTLVESWKSHGDLSSRRSDGYPVLEYI-PENVSSSTLRSVSTGSSRPSKICLV 605
                                                                                                                                                                                                                                                                                                                                                                                          EPPLLPGAYGPPAAPDSLPSTSAAPPGLYSPLGLNGHHQALGFPAAVLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GLPAAPP-PFLGAK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----DLAEYGYPPPDGKEGPFAYG-----EFQSALKIKEEGV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 805; DB 2;
Pred. No. 1.8e-34
59; Mismatches 14
                                                                                                                                                                                                                                               -PYLGYVRPDTETSQS--SQYSFESLPQKICLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -AAPADFAQPPRAGQEPSLE----CVLYKA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      progesterone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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R.J.; G
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A;Cross-references: GB:M68915; GB:J05333; NID:g200471; PIDN:AAA39971.1; R;Hagihara, K.; Wu-Peng, X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W. Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
A;Title: Nucleic acid sequence and DNase-hypersensitive sites of the 5' A;Reference number: I49111; MUID:95100931
A;Accession: I49111
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A;Title: Molecular cloning,
A;Reference number: A39596;
A;Accession: A39596
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A; Residues: 1-9 < HAG>
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A; Residues: 1-923 <SCH>
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C;Date: 20.Mar-1992 #sequence_revision
C;Accession: A35956; 149111
R;Schott, D.R.; Shyamala, G.; Schneider
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C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revisio
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          PEMDGSYFSFMDDK-DYYSLSG-
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30.3%;
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A; Map position: 11q22.1-11q22.3
C; Superfamily: progesterone receptor; erbA transforming protein homology C; Keywords: alternative splicing; DNA binding; nucleus; phosphoprotein; s; F;1-933/Product: progesterone receptor form B #status predicted <MA1>F;165-933/Product: progesterone receptor form A #status predicted <MA2>F;565-829/Domain: erbA transforming protein homology <ERBA>F;567-587/Region: zinc finger CCCC motif
F;603-627/Region: zinc finger CCCC motif
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A;Residues: 1-343,'T','345-933 <KA2>
A;Residues: 1-343,'T','345-933 <KA2>
A;Residues: 1-343,'T','345-933 <KA2>
A;Cross-references: EMBL:X51730; NID:g35651; PIDN:CAA36018.1; PID:g35652
R;Misrahi, M.; Atger, M.; D'Auriol, L.; Loosfelt, H.; Meriel, C.; Fridlansky, Biochem. Biophys. Res. Commun. 143, 740-748, 1987
A;Title: Complete amino acid sequence of the human progesterone receptor deduce A;Reference number; A03245; MUID:87184565
A;Accession: A03245
A;Accession: A03245
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: GB:M15716; NID:g189934; PIDN:AAA60081.1; PID:g189935
C;Genetics:
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C;Accession: S09971; S12464; A03245
C;Accession: S09971; S12464; A03245
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EMBO J. 9, 1603-1614, 1990
A;Title: Two distinct estrogen-regulated
A;Reference number: S09971; MUID:90228361
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A; Residues: 1-933 < KAS>
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Chambon

receptor deduced

steroid

Fri

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F;681-933/Domain: steroid binding #status predicted <STB>
F;41/Binding site: phosphate (Thr) (covalent) #status predicted
F;227,232,552,793/Binding site: phosphate (Ser) (covalent) #status predicted
F;329,374,601/Binding site: phosphate (Tyr) (covalent) #status predicted
```

progesterone receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 20-Aug-1999
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 20-Aug-1999
C;Accession: A25923
R;Loosfelt, H; Atger, M.; Misrahi, M.; Guiochon-Mantel, A.; Meriel, C.; Logeat, F.;
Proc. Natl. Acad. Sci. U.S.A. 83, 9045-9049, 1986
A;Title: Cloning and sequence analysis of rabbit progesterone-receptor complementary
A;Reference number: A25923
A;Accession: A25923
A;Accession: A25923
A;MUID:87067449
A;Residues: 1-930 <LOO>
A;Cross-references: GB:M14547; NID:g165631; PIDN:AAA31443.1; PID:g165632
A;Cross-references: GB:M14547; NID:g165631; PIDN:AAA31443.1; PID:g165632
C;Superfamily: progesterone receptor; erab transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;
F;568-836/Domain: erab transforming protein homology <ERBA>
F;568-588/Region: zinc finger
F;604-628/Region: zinc finger

Qу	Qу Db	Qу	Qy Db	Qу	Qy Db	Qy Db	Qy Db	Db Qy	Фу	Qу	Qy Db	Qу	Qу	Оу	Query Ma Best Loc Matches
828 777	768 717	708 673	649 613	589 555	530 518	482 458	466 398	444 338	426 278	379 223	337 164	286 122	242 72	191 : 20 :	ry Match E Local ches 25
YFAPDLVFNELLARVRE 844 : :: YFAPDLILNEQRMKE 791	TLNRLAGKOMIOVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFL 827 	TTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLS 767 : : : : : : : : : : : : : : : : : : : : : : : : : : : :	KIRRKNCPACRLOKCLQAGMNLGARKSKKLGKLKGIHE-EQPQQQQPPPPPPPPPPPSPEEG 707	LRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIID 648 :	QGTISLSRSARDQSFQHLSSFPPVNTLVESWKSHGDLSSRRSDGYPVLEYI-PENVSSST 588	GNCEGSGFPVGIKQEPDDGSYYPEASIPSSAIVGVNSGGQSFHY-RIGA 529	YYSLSGIGPD 481 :: RSPRSYLVAGANPAAFPDFPLGPPPPLPPRATPSRPGEAAVTAAPASASVSSASSSGST 457	A65 HTVNPFPFMDGSYFSFMDDKD	PTKQES	EVESAISNGYTGQLNIVQYIKPEPDGAFSSSCLGGNSKI-NSDSSFSV 425	VNNAFSYTASGTSAGSSTLRDVVPSPDTQEKGAQEVPFPKTE 378 :	SSPNNVTLRSSVSSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSP 336	ENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPV 285	SPEVGSPLNMTSSVGSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPNA 241	ch 18.1%; Score 801; DB 1; Length 933; al Similarity 29.5%; Pred. No. 3.6e-34; 253; Conservative 95; Mismatches 221; Indels 288; Gaps 37;

RESULT A25923

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               729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHCSVKSPVSSPNNVTLRSSVSSPANINNSRCSVSSPSNTNNRSTLSSP-AASTVGSICS 335
                                                                                                    \tt PTLGLNGLPQLGYQAAVLKEGLPQVYTPYLNYLRPDSEASQSPQYSFESLPQKICLICGD
                                                                                                                                                                                                                         SSGSTLECILYKAEGAPPQQGPFAPLPCKPPGAGACLLPRDGLPSTSASGAAAGAAPALY
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                                                                                                                                                                                                                                                                                                                                                                                                   RVSLAEQDAPVAPGRSPLATSVVDFIHVPILPLNHAFLATRTRQLLEGESYDGGAAAASP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDSSESEGTVGPL-----LKGQPRALGGTAAGGGAAPVASGAAAGGVALVPKEDSRFSAP 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINS-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GAFPGVEAP----
TISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKOMIQVVKWAKVLP
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                                                                                                                                                                                                                                                                                  RSPRTYLVAG----ANPAAFPDFQLAAPPPPSLPPRVPSSRPGEAAVAASPGSASVSSSS
                                                                                                                                                                                                                                                                                                                                                                      ----KGNPTVNPFP-----FMDGSYFSFMDDK-DYYSLSGILGPP-----
                                                                        NLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLS
                                                                                                                                                                                                                                                      GAQGTISL----SRSARDQS--FQHLSSFPP----
                                                                                                                                                                                                                                                                                                           -----VPGFDGNCEGSGFPVGIKQEPDDGSYYPE--ASIPSSAIVGVNSGGOSFHYRI 527
                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IKQES---
                                              VLGGRKFKKFNKVR-VMRALDAVALPQPVGIPNES--QRITF----SPSQEIQLIPPL-
                                                                                                                                                                                             PVL-----
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                                                                                                                                                                                           -----SRPSKICLVCGD 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EGAGDSSSRPPEKD-----SGLLDSVLDTLLAP- 122
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A;Cross-Telectences: EMBL:X33//9; NID:949960; PIDN:CAA3//95.1; PID:949967
A;Caspar, M.L.; Meo. T.; Tosi, M.
Mol. Endocrinol. 4, 1600-1610, 1990
A;Title: Structure and size distribution of the androgen receptor mRNA in will
A;Reference number: A37255; MUID:91133433
A;Accession: A37255
A;Accession: A37255
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-899 <CAS>
A;Cross-references: GB:M37890; NID:9191935; PIDN:AAA37234.1; PID:91936
A;Cross-references: GB:M37890; NID:91935; PIDN:AAA37234.1; PID:91936
A;Cross-references: GB:M37890; NID:91935; PIDN:AAA37234.1; PID:91936
A;Cross-references: GB:M37890; NID:91935; PIDN:AAA37234.1; PID:91936
A;Cross-reference number: A37908
A;Molecule type: mRNA
A;Residues: 1-899 <CHAP.
A;Cross-references: GB:S56585; NID:9236048; PIDN:AAB19916.1; PID:9236049
A;Cross-references: GB:S56585; NID:9236048; PIDN:AAB19916.1; PID:9236049
A;Fitle: The mouse androgen receptor. Functional analysis of the protein and A;Reference number: S17198; MUID:91354214
A;Residues: 1-899 <CHAP.
A;Cross-references: GB:S5932; NID:949968; PIDN:CAA42160.1; PID:949969
A;Accession: S17198
A;Molecule type: MRNA
A;Residues: 1-899 <CFAP.
A;Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A;Accession: S17198
A;Molecule type: mRNA
A;Residues: 1-899 <CFAP.
A;Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A;Accession: S17198
A;Molecule type: mRNA
A;Residues: 1-899 <CFAP.
A;Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A;Accession: S17198
A;Molecule type: mRNA
A;Residues: 1-899 <CFAP.
A;Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A;Accession: S17198
A;Molecule type: mRNA
A;Residues: 1-899 <CFAP.
A;Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A;Accession: S17198
A;Acc
A;Cross-references: EMBL:X53779

R;Gaspar, M.

Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991

A;Title: A single base deletion in the Tfm androgen receptor gen.

A;Reference number: I49501: MUID:92020902

A;Accession: I49501

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-899 <RES>
A;Cross-references: GB:M37890; NID:g191935; PIDN:AAA37234.1; PID

C;Genetics:

A;Introns: 518/2; 569/1; 608/1; 704/1; 752/2; 796/1; 848/3

C;Superfamily: unassigned erbA-related proteins; erbA transformi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: $40626;
A; Accession: $40626
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 366-413 <HEW>
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C;Bate: 31-Oct-1990 #sequence_revision 31-Oct-1990 #text_change 20-Sep-1999
C;Accession: A35895; A37255; A37908; S34398; S17198; S40626; I49501; S12082
R;He, W.W.; Fischer, L.M.; Sun, S.; Bilhartz, D.L.; Zhu, X.; Young, C.Y.F.; K
Biochem. Biophys. Res. Commun. 171, 697-704, 1990
A;Title: Molecular cloning of androgen receptors from divergent species with eptor cDNA probes from dog, guinea pig and clawed frog.
A;Reference number: A35895; MUID:90386642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A35895; MUID:90386642
A; Accession: A35895
A; Molecule type: mRNA
A; Residues: 1-899 <HEA>
A; Cross references: EMBL:X53779; NID:949966;
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       erbA transforming protein
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C:Keywords: DNA binding; transcripti
F;1-536/Domain: regulatory #status p
F;537-795/Domain: erbA transforming
F;539-559/Region: zinc finger
F;575-599/Region: zinc finger
F;650-899/Domain: hormone binding #s
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В
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Best Local
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nes 223; Conserv
                                                                                                                                                                                                                                                                                                   GSSSPSDAGPYAPYGYTRPPQGLTSQESDYSASEVWYPGGVVNRVPYPSPNCVKSEMGPW
FKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE
                                                                         ---ALTPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPG
                                                                                                                                                KSKKLGKLKGIHEEQPQQQQPPPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISR-
                                                                                                                                                                                               HYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGAR
                                                                                                                                                                                                                                                          VESWKS-HGD--LSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGC
                                                                                                                                                                                                                                                                                                                                                                                            DDGSYYPEA - - -
                                                                                                                                                                                                                                                                                                                                                                                                                       GSSGTLEIPSSLSLYKSGALDEAAAYQNRDYYNFPLALSGPPHPPPPTHPHARIKLENPL
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                                                                                                                    KLKKLGNLK-LQEE---
                                                                                                                                                                               HYGALTCGSCKVFFKRAAEGKQKYLCASRNDCTIDKFRKNCPSCRLRKCYEAGMTLGAR
                                                                                                                                                                                                                                                                                                                                                               DYGSAWAAAAAQCRYGDLGSLHGGSVAGPSTGSPPATTSSSWHTLFTAEEGQLYGPGGGG
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                                                           EGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPG
                                                                                                                                                                                                                                         MENYSGPYGDMRLDSTRDHVLPIDYYFP---
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29.0%;
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                                                                                                                                                                                                                                                                                                                                 -LSRSARDQSFQHL-----SSFPPVNTL-----
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Pred. No. 4.7e-32;
0; Mismatches 211;
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Search completed: September 13, 2002, 10:16:58 Job time: 62 sec

This Pcs Bank (uspile)

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Database :
                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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4422
1 METKGYHSLPEGLDMERRWG......FLYFAPDLVFNELLARVREG
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Gapop 10.0 , Gapext 0.5
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SwissProt_40:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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2178.297 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ú	, u	32	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	w	2	_	No.	Result
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NR3 SUBFAMILY.

45	44	43	42	41	40	39	38	37	36	<u>з</u> 5	34
425	427	431.5	436	440.5	445.5	447.5	452.5	452.5	453.5	455.5	455.5
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Q62986 rai	Q9yh32 ore	P57782 one	P06211 rat	P19785 mus	P03372 hor	Q9tv98 equ	Q29040 sus	Q9qzj5 mes	Q91250 poe	P06212 gal	P79373 mag
rattus nor	eochromi	corhynch	rattus norv	s muscul	mo sapie	uus caba	s scrofa	socricet	ephila gi	llus gal	cropus e

ALIGNMENTS

3	င္ပ	င္ပ	CC	CC	S	CC	CC	C	ငင	RL	RT	RΤ	RA	RΑ	RX	ŖΡ	RN ·	Q.	റ്റ	8	SO	GN	DE	Dī	DT	DT	AC.	ID	MCR_I	RESITT
	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,	-!- SUBCELLULAR LOCATION: Nuclear.	LOWER POTASSIUM LEVELS.	AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND	CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TRANSPORT	ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR	-!- FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS	Science 237:268-275(1987).	structural and functional kinship with the glucocorticoid receptor.";	"Cloning of human mineralocorticoid receptor complementary DNA:	Housman D.E., Evans R.M.;	Arriza J.L., Weinberger C., Cerelli G., Glaser T.M., Handelin B.L.,	MEDLINE=87263386; PubMed=3037703;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	NR3C2 OR MLR OR MCR.	Mineralocorticoid receptor (MR).	16-OCT-2001 (Rel. 40, Last annotation update)	01-AUG-1988 (Rel. 08, Last sequence update)	01-AUG-1988 (Rel. 08, Created)	P08235;	MCR_HUMAN STANDARD; PRT; 984 AA.	MCR_HUMAN	· ·

InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLL; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
DOMAIN 1 602 MODULATING. entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial EMBL; M16801; AAA59571.1; -. PIR; A29513; A29513. HSSP; P06536; 1RGD. TRANSFAC; T00513; -.

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RESULT 2
MCR_TUPGB
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ZN_FING
DOMAIN
DOMAIN
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Q29131; Q95268
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                                                                                   DGNCEGSGFPVGIKQEPDDGSYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSAR
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                                                  QKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPPPPSPEGTTYIAPAKEPSVN 720
                                                                                                                                                       KICLYCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRKNCPACRL
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          STANDARD;
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Pred. No. 5.5e-225;
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01-NOV-1997 (Rel. 3
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Mineralocorticoid 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meyer U. Kruhoeffer M., Flugge G., Fuchs E.;
Meyer U. Kruhoeffer M., Flugge G., Fuchs E.;
Meyer U. Kruhoeffer M., Flugge G., Fuchs E.;
PCloning of glucocorticoid receptor and mineralocorticoid receptor only of glucocorticoid receptor and gene expression in the central nervous system of the tree shrew (Tupaia belangeri).";
Brain Res. Mol. Brain Res. 55:243-253(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tupaia glis belangeri (Common tree shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaia.
                                                                                                             DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98250805; PubMed=9582428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9396;
                                                                                                                                                                                                                                                         InterPro; IPR000536; Hormone_; InterPro; IPR001628; zf-C4. Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1. Pfam; PF00105; zf-C4; 1. PRINTS; PR000047; STROIDFINGER
                                                                                                                                                                                                                                                                                                                   EMBL; 275077; CAA99376.1; -. EMBL; X83607; CAA58586.1; -. HSSP; P06536; 1RGD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR_RECEPTOR; Receptor; Transcription regulation; Zinc-finger; Steroid-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
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SM00430; HOLI; 1.
SM00399; ZnF_C4; 1.
                                                             Similarity
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zf-C4.
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91.3%;
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                                                   25;
                                               Score 3985.5;
Pred. No. 7.6e
25; Mismatches
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C4-TYPE.
C4-TYPE.
HINGE.
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RESULT MCR_RAT ID MCR_RAT ID MCF P22 AC P22 
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P22199; Q63763; Q64174;
O1-AUG-1991 (Rel. 19, Created)
O1-AUG-1991 (Rel. 19, Last sequence up
O1-MAR-2002 (Rel. 41, Last annotation
Mineralocorticoid receptor (MR).
     Patel P.D., Sherman T.G., Goldman D.J., Watson S.
"Molecular cloning of a mineralocorticoid (type I complementary DNA from rat hippocampus.";
Mol. Endocrinol. 3:1877-1885(1999).
                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                       STRAIN=SPRAGUE-DAWLEY; TISSUE-Hippocampus; MEDLINE=90114194; PubMed=2558305;
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                            NCBI_TaxID=10116;
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Query Match 88.1
Best Local Similarity 89.1
Matches 746; Conservative
                                                                                                                                                                                                                       TRANSFAC; T00511;
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                               DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
VARSPLIC
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                             EMBL; M36074; AAA41583.1; -.
EMBL; S75686; AAB32663.2; -.
EMBL; S79920; AAB35738.1; -.
PIR; A41401; A41401.
HSSP; P06536; 1RGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloem L.J., Guo C., Pratt J.H.;
"Identification of a splice variant
mineralocorticoid receptor genes.";
J. Steroid Biochem, Mol. Biol. 55:15
-i- FUNCTION: RECEPTOR FOR BOTH MINE
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WISTAR; TISSUE-Cochlea; MEDLINE-95073883; PubMed-7982810; Furuta H., Mori N., Sato C., Hosh Doi K.;
                                                                                                                                                                                   Receptor; Transcription regulation; DNA-binding; Nu
Zinc-finger; Steroid-binding; Alternative splicing
DOMAIN 1 603 MODULATING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridization.";
Hear. Res. 78:175-180(1994).
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SEQUENCE OF 689-787 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOWER POTASSIUM LEVELS.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: TWO FORV
BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERI
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE OR CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND MATER TRANSPORT AND THUS RAISE EXTRACELLULAR FLUID VOLUME AND BLOOD PRESSURE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR3 SUBFAMILY.
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                                                              NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
HINGE.
STEROID-BINDING.
G-> GKCSW (IN SECOND I
A-> G (IN REF. 2).
I-> S (IN REF. 2).
T-> S (IN REF. 2).
T-> S (IN REF. 2).
Score 3919.5;
Pred. No. 2.4e
35; Mismatches
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Csikos T., Tay J., Do Submitted (SEP-1995)
                                                                                                                     Amphibia; Batrachia; Xenopodinae; Xenopus
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                       Xenopus
                                                                                                                                                                                                                  NR3C2
                                                                                                                                                                                                                                      Mineralocorticoid
                                                                                             NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQKCLQAGMNLGARKSKKLGKLKGLHEEQPQQ-----PPPPPPQSPEEGTTYIAPTKEPSV
                                                                                                                                                                                                                  OR MLR.
                                                                                                                                                                                            laevis (African clawed frog)
                                                                                                                                                                                                                                        receptor (MR) (Fragment).
    Danielsen
5) to the
       EMBL/GenBank/DDBJ databases
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Best Local Similarity
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364 736 307

PSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPL | ::|||||||||||||||||| LSAAVILENIEPEIVYAGYDNTQPDTAENLLSSLNQLAGKQMVQVVKWAKVIPGFRNLPL

795

363 735 306

423

KLGKLKGIHEEQPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVNT-ALVPQLSTISRALT GSCKVFFKRAVEGKCSRQHSYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSK

247 621 187

GSCKVFFKRAVEG----

LAQNTLSSRRNDGFPVPGYIPENMSSTTLRSMSTGPSRPSKVCLVCGDEASGCHYGVVTC

-QHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSK

676

246

620 186 565 126

-LSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTC

127 507

> SIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSA-RDQSFQHLSSFPPVNTLVESWKSHGD::|||||||||||||||:::||||||::: FMDGSYFAFMDDKDYYSLSGILGPPVSSFGDGFEGNGFSNQSLNVAIKQETEDSSFYPEN FMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEGSGFP-----VGIKQEPDDGSYYPEA 506 VSLVKFIKPDPDAIFSSTCFG--DTVSSDPAFSIPIKQESCKNTCSSALFKGSQSANPFP

NMPSSAIVGVNSCGQSFHYRIGAQGTISLSRPLNRDQSFQNLSSFPPMSSLVESWKTQSE

452

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67

392 LNIVQYIKPEPDGAFSSSCLGGNSKINSDSSFSVPIKQESTKHSCSGTSFKGNPTVNPFP

Conservative

39.9%; Score 1763.5; DB 1; 72.1%; Pred. No. 1.7e-86; tive 57; Mismatches 51;

Indels

23;

Gaps

80

66 451 Length

612;

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SOFT TITTER WANTER DE LE RESTRETATION DE LE RESTRET
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ZN_FING
ZN_FING
ZN_FING
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000536; Hormone_r
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U15133; AAA75574.1;
EMBL; U15135; AAA75575.1;
HSSP; P06536; 1RGD.
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   SEQUENCE
                                                                                                                                                                                                                                                     Receptor; Tr
Zinc-finger;
                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DO DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING FAMILY.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR BOTH MINERALOCORTICOIDS (MC) SUCH AS ALDOSTERONE AND GLUCOCORTICOIDS (GC) SUCH AS CORTICOSTERONE CORTISOL. THE EFFECT OF MC IS TO INCREASE ION AND WATER TEAN AND THUS RAISE EXTRACELLUIAR FLUID VOLUME AND BLOOD PRESSURE LOWER POTASSIUM LEVELS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NR3 SUBFAMILY
                                                                                                                                                                                                                                                                            SM00430; HOLI; 1.
SM00399; ZNF_C4; 1.
Sp. PS00031; NUCLEAR_RECEPTOR;
Or; Transcription regulation;
                                    <1
229
229
269
269
361
                                                                                                                                                                                                                                                        Steroid-binding
   AA;
                                    228
298
249
293
360
612
      67946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hormone_rec_lig
      MW;
                                                           MODULATING.
NUCLEAR REC
C4-TYPE.
C4-TYPE.
                                 STEROID-BINDING
   CDD66DDC0A5FBA08

    DNA-binding; Nuclear protein;

                                                                                                                                                                  RECEPTOR-TYPE
         CRC64;
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L outstation -
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EDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNELLARVRE EDQITLIQYSWMCLSSFALSWRSYKHASSQFLYFAPDLIFNE--ERMRQ

844

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DOMAIN
CONFLICT
CONFLICT
                                  DNA_BIND
ZN_FING
ZN_FING
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P49844;
                                                                                                                                                                                                                      EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                               modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                    Pfam; PF02155; GCR; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression of the glucocorticoid receptor early embryogenesis of Xenopus laevis."; Biochim. Biophys. Acta 1218:194-198(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                        Receptor;
                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Picard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 452-776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Destree O.H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao X., Kalkhoven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94289478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996
                                                                       DOMAIN
                                                                                                    PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
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A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAII
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                           NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                     GRE TARGET SITE
                                                                                                                                                                                                                    X72211; CAA51010.1;
X77764; CAA54804.1;
P06536; IGDC.
                                                                                                                                                                                                                                                                                                   non-profit institutions as long
                                                                                                                                                                                    IPR001409; Glucortcd_receptor.
IPR000536; Hormone_rec_lig.
IPR001628; zf-C4.
                                                                                        Transcription regulation;
                                                                                 Stero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor (GR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8018720;
E., Peterson-Maduro
  11d-binding.
419
485
440
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480
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502
504
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                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear
MODULATING.
NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
S -> P (IN REF. 2).
T -> A (IN REF. 2).
                                                                                          DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         776
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RESULT 6
GCR_HUMAN
ID GCR_H
AC P0415
DT 01-N0
DT 01-N0
DT 01-MA
DE Gluco
GN NR3C1

NR3C1 OR GRL

GCR_HUMAN STANDARD; PRT; 777 AA PD P04150; P04151; 01-NOV-1986 (Rel. 03, Created) 01-NOV-1986 (Rel. 03, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Glucocorticoid receptor (GR).

update)

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 PLSSMKSSISSP----PSHCSVKSPVSSPNNV----TLRSSVSSPANINNSRCSVSSPS
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            EDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE
                                                     PSPVMVLENIEDEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPL
                                                                                                KLGKLKGIHEEQPQQQQPPPPPPPPPPPQSPEEGTTYIA-PAKEPSVNTALVPQLSTISRALT
                                                                                                                             TAASPGNVNFPNRSVFSNGYSSPGIRSDASPSPSTSSTSTGPPPKLCLVCSDEASGCHYG
                                                                                                                                                                                                                                                                                     -----CEGSGFPVG-IKQEPDD-----
                                                                                                                                                                                                                                                                                                                              NPTVNPFPFMDGSYFSFMDDKDYYSLSGILGPPVPGF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVVPSPDTQEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKDLLKPSSGSPAVRGSPHYNDK-----PGNVIEFFGNYRGGVSVSV---SASCPTSTAS
DDQMTLLQYSWMFLMVFALGWRSYKQTNGSILYFAPDLVITE
                                                                                                                                                                                              -LSSRRSDGYPVLEYIPENVSSSTLRS-----VSTGSSRPSKICLVCGDEASGCHYG
                                                                                                                                                                                                                                                                DHAKDMLLPSADRPISQYKTEKEDYIELCTPGVVNEEKFGPVYCVGNFSGSGLFGNKSSA
                                                                                                                                                                                                                                                                                                           NPWLDP------LFDEQEAFNLLSPLGTGDPFFMKSEVLSEGSKTLSLEDGTQRLG
                                                                                                                                                                                                                                                                                                                                                   FKCDISAQPRPSMGQGGSNGSSSTNLF-----PKDQCTFDLLRDLGISPDSPLDGKS
                                                                                                                                                                                                                                                                                                                                                                                               YMGESDTKVMSSDIAFPSQEQIGISTGETDFSLLEESIANLQAKSLAPDKLIEISEDPGG
                                                                                                                                                                                                                                                                                                                                                                                                                    -----GAQEVPFPKTEEV------ESAISNGVTGQLNIVQYIK-PEPDGA
                                           PTLISLLEVIEPEVLYSGYDSSIPDTTRRLMSSLNMLGGRQVVSAVRWAKAIPGFRNLHL
                                                                                                                                                                                                                     ISVHGVSTSGGQMYHYDL---NTATISQQDVKPVF-NLGS--PGTSIAEGWNRCHGSGND
                                                                                                                                                                                                                                        -----VNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSFPPVNTLVESW-KSHGD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                    ----QQSTTATARESPETSMTRTLVP--ASVAQ-LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 857;
Pred. No. 2
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SEQUENCE FROM N.A.

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MEDLINE-86092206; PubMed-28674/J, Ong E.

Hollenberg S.M., Weinberger C., Ong E.

"hompson E.B., Rosenfeld M.G.

"hompson and expression of
                      VARIANT PHE-753.
MEDLINE-93302771; PubMed-8316249,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Domain structure of human glucocorticoid receptor relationship to the v-erb-A oncogene product."; Nature 318:670-672(1985).
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factor.";
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Hurley D.M., Accili D., St
Rorer E., Constantine K.,
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                                                                                                                                                                  resistance."
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Subramanian S., Martin C.H.;
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phenotypes.";
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SUBCELLULAR LOCATION: Nuclear.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-HGR IS THE PREDOMINANT
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BETA DOES NOT BIND STEROID ITS FUNCTION IS UNCLEAR; HOWEVER, IT
POSSIBLE THAT VARIANT RECEPTORS PERFORM TISSUE-SPECIFIC FUNCTIO
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ZN_FING
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SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
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  TGVSQETSENPGNKTIVPATLPQ
                   PPPPPPQSPEEGTTY IAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYD
                                                     NYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPP
                                                                                                                                                      QGTISLSRSARDQSFQHLSSFPPVNTLVESW----KSHGD--LSSRRSDGYPVLEYIPENV
                                                                                                                                                                            KEDFIELCTPGVIKQE-KLGTVYCQASFPGANIIGNKMSAISVHGVSTSGGQMYHYDM--
                                                                                                                                                                                                                      LSPLAGEDDSFLLEGNSNEDCKPLILPDTKPKIKDNGDLVLSSPSNVTLPQV-----KTE
                                                                                                                                                                                                                                             VNPFPFMDGSYF-----
                                                                                                                                                                                                                                                                                      KPEPDGAFSSSCLGGNSKI--NSDSSFSV-----PIKQESTKHSCSGTSFKGNPT
                                                                                                                                                                                                                                                                                                            LLEESIANLNRSTSVPENPKSSASTAVSAAPTEKEFPKTHSDVSSEQQHLKGQ-----
                                                                                                                                                                                                                                                                                                                                 DVVPS-----PDTQEKGAQ-----
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                                            NYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKGI--
                                                                                     SSPSMRPDVSSPPSSSSTATTGPPPKLCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQH
                                                                                                                                 -NTASLSQQ-QDQK-PIFNVIPPIPVGSENWNRCQGSGDDNLTSLGTLNFPGRTVFSNGY
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/FTIG-VAR_004675.
R -> H (IN GIJTO D -> V
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C4-TYPE.
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G -> GR (IN REF. 3).
; C5C90C9A5DD16AAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_004676.

G -> S (IN GLUCOCORTICOID 50% BINDING AFFINITY).

V -> I (IN GLUCOCORTICOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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STEROID-BINDING.
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V (IN GLUCOCORTICOID
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No. 2.
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.4e-38;
 LTPTLVSLLEVIEPEVLYAGYD
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Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; DFL; 1.
SMART; SM00339; ZnF_C4; 1.
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Q95267;
Q1-NOV-1997
01-NOV-1997
DNA_BIND
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SEQUENCE
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Brain Res. Mol. Brain Res. 55:243-253(1998).

-i- FUNCTION: THE STEROID HORNONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
                                                                                                                                                    PROSITE; PS00031; NUCLEAR_RECEPTOR; Receptor; Transcription regulation; Zinc-finger; Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98250805; PubMed=9582428;
Meyer U., Kruhoeffer M., Flugge G., Fuchs E.;
"Cloning of glucocorticoid receptor and mineralocorticoid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tupaia glis belangeri (Common tree shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z75079; CAA99379.1; -. HSSP; P06536; 1RGD.
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Eukaryota; Metazoa; Chordata;
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01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                 DOMAIN
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SUBCELLULAR LOCATION: Nuclear.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
DOMAIN: TYPTING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA-BINDING DOMAIN AND A C-TERMINAL STERO SIMILARITY: BELONGS TO THE NUCLEAR HORMONE
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Matches
GCR_AOTNA STANDARD; PRT; 7
P79686;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Glucocorticoid receptor (GR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt SDSKQQRLLVDFPKGSVSNVQQPDLSKAVSLSMGLYMGETETKVMGNDLGFPQQGQ-----}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KESLTSPSEEIPSSVHGQERGNVMDFYKTRRGGATVKVFMPSPSLGGSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAQEVPFPKTEEVESAISNGVTGQLNIVQYIKP--EPDGAFSSSCLGGNSKINSDSSFSV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPAKIYONVEQLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAIVKSPIMCH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IKQE-KLGPVYCQANFSGANIIGNKMSAISVHGVSTSGGQMYHYDM---NTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             LSRSARDQSFQHLSSFPPVNTLVESW---KSHGD-----LSSRR--SDGYPVLEY
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                                                                                                                                                   KQASANLLCFAPDLIINE
                                                                                                                                                                            KHTNSQFLYFAPDLVFNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LSEG----NLKEDCKPLILPD---TKPKIKDNGDLILSSPKNV
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4; Mismatches
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ches 222;
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                               update)
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Best Local S
Matches 259
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Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00107; zf-C7; STROIDEINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
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J. Clin. Endocrinol. Metab. 82:465-472(1997).

J. Clin. Endocrinol. Metab. 82:465-472(1997).

THE RECEPTORS ARE INVOLVED INTERPRETATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reynolds P.D., Pittler S.J., Scammell J.G.; "Cloning and expression of the glucocorticoid receptor from squirrel monkey (Salmiri boliviensis boliviensis), a glucoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=37293;
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97176699; PubMed=9024238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001409;
InterPro; IPR000536;
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Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL STEROID-BINDING DOMAIN.

A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRE TARGET SITE
                                             NMTSSVCSPAGINSVSSTTASFGSFPVHSPTTQGTPLTCSPNAENRGSRSHSPAHASNVG 258
                                                                                                                                           QLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAIVKSPIMCHEKSPSVCSPL 198
                                                                                                                                                                                            DFPKGSVSNAQQPDLSKAVSLSMGLYMGETETKVMGNDLGFPQQGQISLSSGETDLQLLE 123
                                                                                                                                                                                                                                                                                          KESLTPGKEENPSSVLTQERGNVMDFSKILRGGATLKVSVSSTSLAAASQSDSKQQRLLV 63
     NRSTSVPE---
                                                                                                                                                                                                                                                                                                                                                                                             259;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
421
457
487
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528
777 i
                                                                                                                                                                                                                                            -TELESKELSATVAESMGLYM----DSVRDADYSYEQQNQQGSMSPAKIYQNVE 138
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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     -NPKSSASSVSAAP
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C4-TYPE.
HINGE.
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Pred. No. 3.5e-38;
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8E2001875D184203
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               KEKEFPKTE--
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RESULT 9
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Glucocorticoid receptor (GR).
NR3C1 OR GRL.
                                                                                        Reynolds P.D., Pittler S.J., Scammell J.G.; "Cloning and expression of the glucocorticoid receptor squirrel monkey (Saimiri boliviensis boliviensis), a gl
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
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                                                                                                                                   MEDLINE=97176699; PubMed=9024238;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=39432;
                                                                                                                                                                                                                                Saimiri boliviensis boliviensis (Bolivian squirrel monkey).
                                                                J. Clin. Endocrinol. Metab.
                                                                                                                                                   TISSUE-Liver;
                                                                              resistant primate.";
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                     PROCESSION OF THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
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LOCATION: Nuclear
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Best Local Similarity
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InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
Pfam; PF00155; GCR; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLL; 1.
SMART; SM00430; HOLL; 1.
SMART; SM00439; ZnF_C4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict the European Bioinformatics institute.
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                        HSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEGSGFPVGI
                                                                          PKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINSDSSFSVP-IKQESTK
                                                                                                   NQSPWKSDLLIDENCLLSPLAGEEDSFLLEGNSN---
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C4-TYPE.
C4-TYPE.
HINGE.
STEROID-BINDING.
STEROID-BINDING.
W; CE3CD9E8D6A4F3AB CRC6
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Pred.
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No. 3.5e-38;
EDFIELC----
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                                                   --- NGDLYLSSSSNVTLPQVKTEK--
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                        Mol.
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                                                                                                                                                                                                                                                Keightley M.C., Fuller P.J.;

MOL. Endoorinol. 8:731-731(1994).

MOL. Endoorinol. 8:731-731(1994).

THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
                                                                                                                                                                                                                                                                                                                                                      Keightley M.C., Fuller P.J.; "Induce sequences in the guinea pig glucocorticoid receptor induce "Unique sequences in the guinea pig glucocorticoid sensitivity."; constitutive transactivation and decrease steroid sensitivity."; Mol. Endocrinol. 8:431-439(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucocorticoid receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10141;
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                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                             ERRATUM
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                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRE TARGET SITE.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPQSPEEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SVSTGSS-RPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-\texttt{PIFNVIPPIPVGSENWNRCQGSGDDNLTSLGTLNFPGRTVFSNGYSSPSMRPDVSSPP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFQHLSSFPPVNTLVESW---KSHGD--LSSRRSDGYPVLEYIPENVSSSTLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLNRLAGKOMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSOFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGVSQETSENPANKTIVP--ATLPQ-LTPTLVSLLEVIEPEVLYAGYDSTVPDSTWRIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYIA-PAKEPSVNTALVPQLSTISRALTPSPVNVLENIEPEIVYAGYDSSKPDTAENLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSSTATTGPPPKLCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFAPDLVFNE 837
                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
L13196; AAA61612.1; P06536; 1GDC.
                                                                                                                                                               SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                      institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Hystricognathi; Caviic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771
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                                                                                                         There are no
                                                                                         as its content
                                                                            Usage
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                                                                                                       restrictions on
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Best Local
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Pfam; PF00104; hormone_rec; 1.

Pfam; PF00105; zf-C4; 1.

Pfam; PF00105; zf-C4; 1.

Pfam; PF00047; STROIDFINGER.

SMART; SM00430; HOLI; 1.

SMART; SM0039; ZnF_C4; 1.

SMART; SM0039; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001409; Glucortcd_receptor.
InterPro; IPR000536; Hormone_rec_lig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEVPSSVLGSERR-----NVIDFYKTVRGGATVKVSASSPSLAAAAQSDSKQRR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQAVERSSLGPTERTDENNYMEIVNVSCVSGAIPNNSTQGSSKEKQELLPCLQQDNNRPG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILTSDIK---TELESKELSATVAESMGLYM----DSVRDADYSYEQQNQQGSMSPAKIYQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLVDFPKGSGSNAQQPDLSKAVSLSMGLYMGETETKVMGNDLGFPQQGQISLPSGETDFR 119
                                                                                                                                                                                                                                            KGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINSDSSFSVP
                                                                                                                                                                                                                                                                                           SVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVVP---SPDTQE
                                                                                                                                                                                                                                                                                                                    ----SDLSSEQENLKSQAGT--NGGNVKFP---PDQSTFDILKDLEFSSGSPGKERSE--
                                                                                                                                                                                                                                                                                                                                SNVGSPLSSMKSSISSPDSHCSVKSPVSSDNNVT-----LRSSVSSPANINNSRC
                                                                                                                                                                                                                                                                                                                                                                    ENPKNSASAV------
                                                                                                                                                                                                                                                                                                                                                                                        -SPLNMTSSVCSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPNAENRGSRSHSPAHA
                                                                                                                                                                                                                                                                      SPWRPDLLMDESCLLSPLAGE ---
NDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPP
                                                                                               SRSARDQSFQHLSSFPPVNTLVESW-----KSHGDLSSRRSDGYPVLEYIPENVSSSTLR
                                                                                                                                              SGFPVGIKQEPDDGSYYPEASIPSSAIVG------VNSGGQSFHYRIGAQGTISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267;
                          PDVSSPPSSSTTTGPPPKLCLVCSDELSGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGR
                                                                        SQQ-QDQK-PIFNVIPPIPVGSENWNRCQGSGEDNLTSLGTVNFPGRSVFSNGYSSPGLR
                                                                                                                       ----IKQE-KLGPYYCQASFSGANIIGNKMSAISVHGVSTSGGQMYHYDM---NTASL
                                                                                                                                                                        IGKEDFIELCT - - -
                                                                                                                                                                                             IKQESTKHSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYSLSGTLGPPVPGFDGNCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                        -----SVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGR
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416
452
482
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481
436
476
771
51
406
666
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zf-C4.
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                                                                                                                                                                                                                         ------IKDNGDGILSSS-----NSVPQPQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR RECEPTOR
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
POLY-ALA.
POLY-SER.
POLY-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 850.5;
Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4C0710E9C980F09E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 224;
                                                                                                                                                                                                                                                                       --DDPF-----LLEGNSN-EDCKPLILPDTKP
                                                                                                                                                                                                                                                                                                                                                                      ----SGTPTEEFPKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.7e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                             -PGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279;
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RESULT
GCR_PIG
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Q9N1U3; Q9GK
16-OCT-2001
 DOMAIN
DNA_BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Porcine glucocorticoid receptor sequencing, cloning, recombinante expression and raising a antiserum. *;

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: THE STERCID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
                                                                                                                                                                    Pfam; PF02155; GCR; 1.
Pfam; PF00104; hormone_rec;
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                          SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4;
                                                                                                                                        PRINTS; PR00398; STRDHORMONER. PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              EMBL; AF141371; AAF66595.1; -. EMBL; AJ296022; CAC10271.1; -.
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict the property of the swiss as long as its content is used by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gutscher M., Eder S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucocorticoid receptor
                                                             Receptor; Tr
Zinc-finger;
                                                                                           PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                 InterPro; IPR001409; Glucortcd_receptor.
InterPro; IPR001536; Hormone_rec_lig.
InterPro; IPR001723; Strdhormone_receptor
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NR3C1 OR GRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear (By similarity).

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATION OF THREE DOMAINS: A MODULATION OF THREE DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRE TARGET SITE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR3 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GKZ9;
                                                                           Transcription regulation;
   385
385
                                                             Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
   384
450
405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller M., Claus R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GR) (Fragment).
MODULATING.
NUCLEAR RECEPTOR-TYPE
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                           1.
DNA-binding;
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                                                                             Nuclear
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tent is in no
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                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration
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            QYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE 837
QYSWMFLMVFALGWRSYRQSSASLLCFAPDLVINE
                                                                                                                      IHEEQPQQQQPPPPPPPPQSPEEGTTYIA-PAKEPSVNTALVPQLSTISRALTPSPVMVL
                                                                                                                                                                     KVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKG
                                                                                                                                                                                                          FSGRSVFSNGYSSPGMRPDVSSPPSSSSAATGP--PPKLCLVCSDEASGCHYGVLTCGSC
                                                                                                                                                                                                                       LSSRR--SDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSC
                                                                                                                                                                                                                                                                                                                                                                                         CLGGNSKINSDSSFSVPIKQESTKHSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAAVSQPDSKQQRLAVDFPKGSGSNAQQPDLSKAVSLSMGLYMGETETKVMGSDLGFPQQ 67
                                                  EVIEPEVLYAGYDSSIPDSTWRIMTALNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLL
                                                              ENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLI
                                                                                                                                                        KVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKG
                                                                                                                                                                                                                                                           GGQLYHYDMNTAASLSKQQEQKPL----FNVIPPIPVGSENWNRCQGSGDDNLTSLGTLN
                                                                                                                                                                                                                                                                                    GGQSFHYRIGAQGTISLSRSARDQSFQHLSSFPPVNTLVESW---KSHGD------
                                                                                                                                                                                                                                                                                                                                        SGILGPPVPGFDGNCEGSGFPVGIKQEPDDGSYYPEASIPSSAIVG------VNS
                                                                                                                                                                                                                                                                                                                                                                                                                    SST-EDCKPLVLPDTK-----PKVKD-----NG-----ELILPSPN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTLRDVVP--SPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIWRKKLQDLELPSGSPGKETSESPWSSDLLIDENCLLSPL-----AGEEDPFLLEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPV-SSPNNVTLRSSVSSPA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPIMCHEKSPSVCSPLNMTSSVCSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPNAE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQQGSMSPAKIYQNVEQLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAIVK 182
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491
>703
                                                                                                                                                                                                                                                                                                                                                                  SVPLPQVKT-----
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31.2%;
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HINGE.
STEROID-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
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No. 6.1
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595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                  -----EKEDFIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                    623
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                                                                                                                                                                                                                                                                                                                                                                                                                     233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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RESULT 12 GCK_SAGOE STANDARD; ID GCK_SAGOE STANDARD; AC P79269; DT 01-NOV-1997 (Rel. 35, Created)

PRT;

777

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Best Local S
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16-OCT-2001 (Rel. 40, Last annotation
Glucocorticoid receptor (GR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saguinus oedipus (Cotton-top tamarin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
NCBI_TaxID=9490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistant primate.";

J. Clin. Endocrinol. Metab. 82:465-472(1997).

-i. FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN

-i. FUNCTION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE GRE TARGET SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97176699; PubMed-9024238;
Reynolds P.D., Pittler S.J., Scammell J.G.;
"Cloning and expression of the glucocorticoid receptor
squirrel monkey (Saimiri boliviensis boliviensis), a gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NR3C1 OR GRL.
                                                                                                                                                                                                                                                                                         DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02155; GCR; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U87953; AAC51133.1; -. HSSP; P06536; 1GDC.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001409; Glucortcd_receptor.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00031; NUCLEAR_RECEPTOR;
110
                           139 QLVKFYKGNGHRPSTLSCVNTPLRSFMSDSGSSVNGGVMRAIVKSPIMCHEKSPSVCSPL 198
                                                            64
                                                                                        98
                                                                                                                                                 28 RSSLGPTERTDENNYM--EIVNVSCVSGAIPNNSTQGSSKEKQELLPCLQQDNNRPGILT 85
                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NR3
                                                                                                                    KESLTPGKEENPSSVLTQERGNVMDFCKILRGGATLKVSVSSTSLAAASQSDSKQQRLLV 63
                                                            DFPKGSVSNAQQPDLSKAVSLSMGLYMGETETKVMGNDLGFPQQGQ
                                                                                        SDIK---TELESKELSATVAESMGLYM----DSVRDADYSYEQQNQQGSMSPAKIYQNVE
                                                                                                                                                                                   259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation;
                                                                                                                                                                                                                                                            421
421
457
487
487
528
777
                                                                                                                                                                                   Conservative 103;
                                                                                                                                                                                                                                                                                                                                                                    Steroid-binding.
                                                                                                                                                                                                                                                              AA;
 ISLSSGETDLQ-LLEESIANLN-
                                                                                                                                                                                                                                                                            420
486
441
441
481
527
777
                                                                                                                                                                                                                                                              85593 MW;
                                                                                                                                                                                                   19.1%;
                                                                                                                                                                                                                                                           NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
HINGE.
STEROID-BINDING.
STEROID-BINDING.
E4F9D24AEC5F9D58 CRC64;
                                                                                                                                                                                   score 845; DB 1;
Pred. No. 9.3e-38;
3; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                        MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                         1.
DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                Length 777;
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                                                                                                                                                                                      Indels
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    RSTSV--PE 137
                                                                                                                                                                                        260;
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                                                                                                                                                                                    Gaps
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RP				R R				3 8								ID	GCR_MO	BECIII	ţ	7	Qy	בט	!	УО	Db	ļ	Оу	Дb	67	Ov	Db	Qy	Ę	D _b	Qy	Дb	Qy	Db	Qy	מע	2	Qy	Db	Qy	מט	2 5)	Db	Qy
SEQUENCE OF 1-755 FROM N.A. MEDLINE-89098404; PubMed=2911477;	on 1 755 EDOM N	proteins."; EMBO J. 5:2513-2522(1986).	sequencing and expression of wild-type	eceptor: mapping of functional do	Med=3/80669;	FROM N.A.	[1]	ndentia: Sciurognathi: Muridae; Murinae;	ordata: Craniata: Vel	MIN THEORY OF CALLET	NESTA OF CET OF CET (2007)	coid recentor (GR)	o (Rel. 00, Last sequence o	o (mal of last sections in	P06537; Q61628; Q61629;	GCR_MOUSE STANDARD; PRT; 783 AA.	JSE 13	_		≥ -	829 FAPDLVFNE 837	563 LNMLGGKQVIAAVAWAAAIFGEAMBIIBDOQIIIBBAACIIII DIII)	769 LNRLAGKOMIOVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSOFLY	506 GVSQETSENPANKTIVPATLEQ-LTETHVSHLEVIEFEVLINGIDGIVEDSIVE	:: ::	QLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDJ	468 IRRKNCPACRYRKCLQAGMNLEARKTKKKIKGI	- ;	650 TRRKNCPACRLOKCLOAGMNLGARKSKKLGKLKGTHEEQPQQQQPPPPPPPPPQSPEEGTT	STATTGPPPKLCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIID	591 SVSTGSS-RPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGKNUC11Dx		349 -PIFNVIPPIPVGSENWNRCQGSGDDNLTSLGTLNFPGRTVFSNGYSSPSMRPDVSSPPS	544 FQHLSSFPPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSTLR	KLSTVYCQASFPGANIIGNKMSAISIHGVSTSGGQMYHYDM	1	- TPGV	GILGPPYPGEDGNCEGSGEFYG	00 NINUTERS 000 NI	::	376 KTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINSDSSFSVP-IKQESTKH	LAGEEDSFLLEGNSNEDCKPLILP	NAFSYTASGTSAGSSTLRDVVPSPDTQEKGAQEVPF		SO SEPREPARATION OF STREET CONTROL OF STREET CON	EO GDI GGDI GGWYGG	138 NPKSSASSSVSA	199 NMTSSVCSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPNAENRGSRSHSPAHASNVG
			ř	γď																			62	82		η Λ	761	Ö	•	709	46		_	407	59(348	4		, ,	ò	280	434	255	7 / 5	í	ö	318	149	258

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Best Local :
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CONFLICT
SEQUENCE
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ZN_FING
ZN_FING
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRE TARGET SITE.

-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL D A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; zinc-finger; Steroid-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00430; HOLI; 1
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T00335; ...
MGD; MGI:95824; Nr3c1.
InterPro; IPR001409; Glucortcd_receptor.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X04435; CAA28031.1; -. EMBL; X13358; CAA31738.1; -. EMBL; X13359; CAA31739.1; -. EMBL; X13359; CAA51739.1; -. EMBL; A25691; A25691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids Res. 17:445-445(1989).
-- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nohno T.,
                213
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                                                                                                                                                                                    46 VNVSCVSGAIPNNSTQGSSKEKQELLPC------LQQDNNRPGILTSDIKTELESKE 96
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VSSTTASFGSFPVHSPITQGTPLTCSPNAENRGSRSHSPAHASNVGSPLSSPLSSPLSSMKSSI
                                                                                                                  LSATVAESMGLYM----DSVRDADYSYEQQNQQGSMSPAKIYQNVEQLVKFYKGNGHRPS 152
                                                                                                                                                       VKVSASSPSVA-AASQADSKQQRILLDFSKGSASNAQQQQQQQQP-----QPD
                                                                                              TLSCVNTPLRSFMSDSGSSVNGGVMRAIVKSPIMCHEKSPSVCSPLNMTSSVCSPAGINS
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                                                                                                                                                                                                                                                                                                     ; Steroid-binding; A

1 427 MC

428 493 NC

428 448 C4

464 488 C4

464 783 ST

75 PC

458 458 G

437 437 V
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30.6%;
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possibly
receptor
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                                                                                                                                                                                                                                                                                    NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
POLY-GLN.
G -> GR (IN ISOFORM B).
V -> G (IN REF. 2).
W; 455E5CIC3C955E2A CRC64;
                                                                                                                                                                                                                                Score 842;
Pred. No. 1
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                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                             DB 1;
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RR	RESULT GCR_RAT ID GCP AC POID DT 01- DT 01- DT 16- DE GL GN NR3 OS RAT OC MAIN OX NCE	Db Qy Db		Qy Db Qy	Qy Qy Db	מם עע מס	o de dy	Db Db
SEQUENCE FROM N.A. TISSUE=Hepatoma; MEDLINE=86272086; PubMed=3755378; Miesfeld R., Rusconi S., Godowski P.J., Maler B.A., Okret S., Wikstroem AC., Gustafsson JA., Yamamoto K.R.; "Genetic complementation of a glucocorticoid receptor deficiency by expression of cloned receptor cDNA.";	LRAT 536; JAN-19 NOV-19 NOV-10 CCT-20 CCT-20 CCT-20 CT-20 CT	566 MTTLMMLGGRQVIAAVKMAKAIPGFRNLHLDDQMTLLQYSMMFLMAFALGWRSYRQASGN 625 826 FLYFAPDLVFNE 837 	EGTTYIAPAKEPSVNTALVPOLSTISRALTPSPVMVLENIEPEIVYAGYDSSKPDTAENL 7	586 SSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKVEFKRAVEGQHNVLCAGRNDC 645	492 GIKQEPDDGSYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSAR 540	63 -PKIQDT	22 LSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRDVVPSPDTQEKGAQEV	149 KSSTPAAGCATPTEKEFPQTHSDPSSEQQNRKS 181 273 SSPPSHCSVKSPVSSPNNTLRSSVSSPANI-NNSRCSVSSPSNTNNRS

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a study and of t vitro.";
Baumann H., Paulsen R
Gustafsson J.-A., Hae
"Refined solution str
domain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lanz R.B., Hug M., Gola M. "Active, interactive, and Steroids 59:148-152(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Zinc finger mutations that alter glucocorticoid receptor."; J. Mol. Biol. 230:124-136(1993).
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Prostate;
MEDLINE-88067783; PubMed=3684608;
                                                                                                                                                                                                                                                                                                                                                                       Science
[9]
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                                                                                                                                    MEDLINE=92038072; PubMed=1936288; Kellenbach E., Maler B.A., Yamamoto K.R., Boelens R., Kaptein R.; "Identification of the metal coordinating residues in the DNA binding domain of the glucocorticoid receptor by 113Cd-1H heteronuclear NMR spectroscov"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
[8]
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MEDLINE-91326070; PubMed=1865905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93195921; Pozandi E., Galli I.,
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                                                       SINUCTURE BY NMR MEDLINE=94079877;
                                                                                                                                                                                                                                                                    Remerowski M.L., Kellenbach E., Boelens R., van der Marel A.,
van Boom J.H., Maler B.A., Yamamoto K.R., Kaptein R.;
"1H NMR studies of DNA recognition by the glucocorticoid receptor:
complex of the DNA binding domain with a half-site response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystallographic analysis of the receptor with DNA.";
                                                                                                               spectroscopy.";
FEBS Lett. 291:367-370(1991).
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                                                                                                                                                                                                                                             Biochemistry
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binding 'finger' structures in t
by site-directed mutagenesis.";
7:2503-2508(1988).
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enbach E., Boelens R., Maler B.A.,
Carlstedt-Duke J., Yamamoto K.R.,
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                                   en K.,
Haerd
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Gustafsson
                       receptor DNA-binding
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InterPro;
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SMART; SM00399; ZnF_C
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pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFING
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Receptor; Transcription regulation; DNA-binding; Nuclear protein;
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FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
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Y12264;

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DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING NO-THREE DOMAIN
A DANA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAI
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
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IPR000536; Hormone_rec_lig.
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CAA68545.1;
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S -> G.
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                                                                                                                                                                                                                SDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKVFFKRA
                                                                                                                      QQQPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIV
                                                                                                                                                               VEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQ
                                                                                                                                                                                                    SNGYSSPGMRPDVSSPPSSSSAATGP--PPKLCLVCSDEASGCHYGVLTCGSCKVFFKRA
                                                                                                                                                                                                                                                      DM---NTASLSQQ-QDQK-PVFNVIPPIPVGSENWNRCQGSGEDSLTSLGALNFPGRSVF
                                                                                                                                                                                                                                                                             RIGAQGTISLSRSARDQSFQHLSSFPPVNTLVESWK-----SHGDLS----SRR
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                       SFALSWRSYKHTNSQFLYFAPDLVFNE
                                                YAGYDSSVPDSAWRIMTTLNMLGGRQVIAAVKWAKAILGLRNLHLDDQMTLLQYSWMFLM
                                                                         YAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLS
                                                                                                  VSQ--
                                                                                                                                                  VEGQHNYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK--KIKGIQQATAG
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Pred. No. 1.5e
89; Mismatches
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RESULT 15
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ID GCR_SA

GCR_SAISC

STANDARD;

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Matches

Conservative

104;

Indels

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Gaps

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28 RSSLGPTERTDENNYM--EIVNVSCVSGAIPNNSTQGSSKEKQELLPCLQQDNNRPGILT

KESLTPGKEENPSSYLTQERGNVMDFCKILRGGATLKVSVSSTSLAAASQSDSKQQRLLV

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Query Match
Best Local
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15-JUL-1999
15-JUL-1999
16-OCT-2001
                                                                  DOMAIN
CONFLICT
SEQUENCE
                                                                                                                          DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-i - FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED

-i - FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED

-i - FUNCTION: AND OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR

PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Scammell J.G., Denny W.B., Valentine D.L.;

**Over-expression of the fk506-binding immunophilin common cause of glucocorticoid resistance in three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saim
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                               SMART; SM00430;
SMART; SM00399;
                                                                                                                                                                                                                                                       pfam; PF02155; GCR; 1.
pfam; PF00104; hormone_rec; 1.
pfam; PF00105; zf-C4; 1.
pRINTS; PR00047; STROIDFINGER.
                                                                                                                DOMAIN
                                                                                                                                                                                   Zinc-finger;
                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                            InterPro; IPR001409;
InterPro; IPR000536;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DUA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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P06536; 1GDC
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el monkey (
           Similarity
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(Rel. 38, Last sequence update)
(Rel. 40, Last annotation updat
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421
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                                                                    HINGE.
STEROID-BINDING.
MISSING (IN REF. 2).
721B8203939D1389 C
Score 840.5; Pred. No. 1.6e
                                                                                                                          C4-TYPE.
                                                                                                                                                        NUCLEAR
                                                                                                                                                                        MODULATING
                                                                                                                                                                                               DNA-binding; Nuclear protein;
                                                                                                                                                          RECEPTOR-TYPE
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5; DB 1;
1.6e-37;
hes 227;
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                                                                                                                                                                                                                                                                                                     HSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEGSGFPVGI 493
                                                                                                                                                                                                                                                                                                                                           PKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINSDSSFSVP-IKQESTK 433
                                                                                                                                                                                                                                                                                                                                                                                          NRSTLSSPAASTVGSICSPV-NNAFSYTASGTSAGSSTLRDVVP--SPDTQEKGAQEVPF 374
                                                                                                                                                                                                                                                                                                                                                                                                               SDYSSEQQNLKGQTG------TNGGNYKLYTADQSTFDILQDLEFSSGSPGKET
                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSVSSPANI-NNSRCSVSSPSNTN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRSTSVPE----NPKSSASSSVSAAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMTSSVCSPAGINSVSSTTASFGSFPVHSPITQGTPLTCSPNAENRGSRSHSPAHASNVG 258
                                                                             -SVSTGSS-RDSKICLYCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIID 648
                                                                                                                                                                                                       K-PIFNVIPPIPVGSENWNRCQGSGDDNLTSLGTLNFPGRTVFSNGYSSPSMRPDVSSPP 406
                                                                                                                                                                                                                          SFQHLSSFPPVNTLVESW---KSHGD--LSSRRSDGYPVLEYIPENVSSSTLR-----
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                                                  TLNRLAGKQMIQVVKWAKVLPGFKNLFLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFL
                                                                                                                                   KIRRKNCPACRLOKCLOAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPPPQSPEEGT 708
CFAPDLIINE 632
            YFAPDLVFNE 837
                                       TLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQASSNLL
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Search completed: September 13, 2002, 10:21:51 Job time: 290 sec

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Result
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Q9ddu9 xenopus lae
Q90zm7 petromyzon
Q9glw0 canis famil
Q9dev4 xenopus lae
Q9jbd5 anguilla ja
Q93245 oncorhynchu
Q9gk17 sus scrofa
Q42274 crocodylus
Q9jac6 oncorhynchu
Q9gkp9 sus scrofa
P70048 xenopus lae
Q9un21 homo sapien
Q9yqy9 anguilla ja
Q9pwg5 anguilla ja
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Q96kq9 homo sapien
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8MON6

PRELIMINARY;

PRT;

982 δ

01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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400.5	401.5	406.5	410.5	412	414	420	422	422	422.5	429.5	434	446.5	449.5	457.5	486	495.5	529	539.5	602.5	634.5	638.5	644.5	669.5	708	709.5	714.5	716.5	719.5
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QYSMEY	090WS9	Q95JC0	Q90WH6	Q90WV1	Q98SM9	Q98SM7	Q9BDW5	Q95MF0	Q923G6	Q95L13	090WS8	090ZM8	Q91698	Q90ZC2	Q918F5	Q28547	Q9вDJ7	Q9IA30	090Y00	Q91425	Q9W6F4	Q91445	097684	Q13771	093244	Q9DDJ4	090ZM6	093497
Q95me9 callithrix		Q95jc0 canis famil	Q90wh6 clarias gar	Q90wv1 carassius a	Q98sm9 brachydanio	7	Q9bdw5 sus scrofa	Q95mf0 macaca arct	Q923g6 mesocricetu	0	-		Q91698 xenopus lae		Q9i8f5 pimephales	0	Q9bdj7 ovis aries	O			Q9w6f4 haplochromi	ser		Q13771 homo sapien			petromy	093497 pagrus majo

ALIGNMENTS

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Query Match
Best Local Similarity
Matches 818; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               MINERALOCORPICOID RECEPTOR
Saimiri sciureus (Common squirrel monkey)
Fikarvota; Metazoa; Chordata; Craniata; V
                                                                                                                                                                                                                                                                  "Squirrel Monkey Mineralocorticoid Receptor cDNA.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; AF245224; AAF63382.1; -.
HSSP; P06536; IRGD.
                                                                                                                   PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                          Zinc-finger
SEQUENCE
                                                                                                                                                                                          InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-c4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-c4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
                                                                                                DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                       InterPro; IPR000536; Hormone_rec_lig
                                                                                                                                                                                                                                                                                                                                                              Patel P.D.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                         982 AA;
   Conservative
                                                                            107084 MW;
               96.48;
97.78;
Score 4262; DB 6;
Pred. No. 1.2e-279;
3; Mismatches 14;
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                            Length 982;
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O96KQ9;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence up
O1-DEC-2001 (TrEMBLrel. 19, Last annotation
MINERALOCORTICOID RECEPTOR DELTA.
                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                               Homo
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SEQUENCE
            NCBI_TaxID-9606;
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                                                                                                        SSESVPTKQESTKHSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYSLSGILGPPVPGF
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                               (Human)
                   Chordata;
Primates;
                   Craniata; Vertebrata; Catarrhini; Hominidae;
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                    Hominidae;
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SEQUENCE
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                     Q9DDU9;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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| QKCLQAGMNLGERR
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                                                                                                                                                                                                                                                                                                                                                                                                                                  670;
                                                                                                                                                      DQSFQHLSSFPPVNTLYESWKSHGDLSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPS
                                                                                                                                                                                                                                 SPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSSCLGGNSKINSD
                                                                                                                 KICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRL
                                                                                                                         KICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRL 660
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               (TremBLrel. (TremBLrel. (TremBLrel. ETTEMBLrel. TRECEPTOR.
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19,
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Pred. No. 2.4e
2; Mismatches
                       Last sequence up
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Query Match
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SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tian J., Kim S., Heilig E., Ruderman J.V.;
"Identification of XPR-1, a progesterone receptor required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02161; Prog_receptor; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oocyte activation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein;
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Xenopodinae; Xenopus.
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AGRNDCIIDKIRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPP
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                                                                                                                                    GAQGTISLSRSARDQSFQHLSSFPPVNTLVESWKSHGDL---SSRRSDGYPVLEYIPENV
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Pro; IPR000128; Progest_receptor.
Pro; IPR001723; Strdhormone_receptor.
Pro; IPR001628; zf-C4.
PR00164; hormone_rec; 1.
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                                                                                                                                                                                                                                                                                                           -SPDTFQ---TSIPYANLQP-----NMKQISYFYPDTQPDF---
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                                                                                                    HQHI-TFQP-TSMKETYLSEIQLPYVSYIRSDGNP-----
                                                     -SRPSKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLC
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Pred. No. 2.6e
94; Mismatches
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                                                                                                                                                                      --CVLPSTS-----AQTIYQPL
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01-DEC-2001 (TrembLrel. 19, C
01-DEC-2001 (TrembLrel. 19, L
01-DEC-2001 (TrembLrel. 19, L
CORTICOID RECEPTOR (FRAGMENT)
  Q9GLW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evolution of vertebrate steroid receptors from an ancestral receptor by ligand exploitation and serial genome expansions. Proc. Natl. Acad. Sci. U.S.A. 98:5671-5676(2001).

EMBL; AY028457; AAK20930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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49.8%;
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01-MAR-2001
01-MAR-2001
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-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
BMBL, AF177470; AAG09282.1; -.
HSSP; P06401; 1A28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR000128; Progest_receptor.
InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
pfam; PF00104; hormone_rec; 1.
pfam; PF00161; Prog_receptor; 1.
pfam; PF00165; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and cellular progesterone receptor."; Submitted (AUG-1999) to the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
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                                                                                                                                                                                                                           GTSAGSSTLRDVVPSPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAF
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                                                                                                                          NPFPFMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEGSGFPVGIKQEPDDGSYYPEAS
                      HGDLSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGS
                                                                                                                                                                                                      GDFPDCAYPSDAEPKDDA-----FPLYGDFQPPALK--
                                                                                                                                                                                                                                                       TMMDFIHVPILPLGSAFLAARTRQLLEAETYDAGAFAPPRGSP-SAPCAPL----
                                                                                                                                                                                                                                                                               TLRSSVSSP----ANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTAS
                                                                                                   SPGPALECV-----LYKAEGAPPPQGPFAAAPCRVPG--AGACLLPRDGA---
                                                                                                                                                    AAARSPRPYLAAGPHSCVFADAPPALPALPPLPPRAPSSRPGEGAPAAAAAAAGCSASSAS
                                                                                                                                                                           SSS-----CLGGNSKINSDSSFSVPIKQESTKHSCSGTSFKGNPTV----
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Carnivora; Fissipedia;
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                                                                       -GQSFHYRIGAQGTISLSRSARDQSFQHLSSFPPVNTLVESWKS
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lular localization
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Last sequence update)
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Pred. No. 2.
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ia; Canidae;
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Canis.
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Bayaa M., Booth R.A., Sheng Y., Liu X.J.;
Bayaa M., Booth R.A., Sheng Y., Liu X.J.;
Pric classical progesterone receptor mediates xenopus oocyte maturation through a nongenomic mechanism.";
Proc. Natl. Acad. Sci. U.S.A. 97:12607-12612(2000).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; AY007198; AAG01366.1; T.
HSSP; P06535; 1RGD.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000128; Progest_receptor.
InterPro; IPR000128; Progest_receptor.
InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
Piam; pf00104; hormone_rec; 1.
Piam; pr00104; hormone_rec; 2.
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01-MAR-2001
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01-DEC-2001
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                                                                                                                                                                                                                                     DNA-binding; Nuclear protein;
Zinc-finger.
                                                                                                                                                                                                                                                             pfam; pF02161; prog_receptor; 2.
pfam; pF00105; zf-C4; 1.
prints; pr00398; sTRDHORMONER.
prints; pr00047; STRDHORMORER.
prints; pr00047; STROHDFINGER.
smart; sm0039; InF_C4; 1.
smart; sm00391; InF_C4; 1.
pr05ITE; pS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593
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                                                                                                                             SPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPE--PDGAFSSSCLGGNSKIN 418
                                                                    SDSS----FSVPIKQESTKHSCSGTSFKGNPTVNPFPFMDGSYFSFMDDKDYYSLSGTLG 474
                      PPVPGFDGNCEGSGFPVGIKQEPDDGSYYPEASIPSSAIVGVNSGGQSFHYRIGAQG--T
                                                  KDSSIVSLYKVAAK-ESTLCQDYGSSPRNPSTPDTDPSLDFILYK-NEDYDCFKIS----
                                                                                                       SPDTSQ-
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1 (TrEMBLrel. 16, 1
1 (TrEMBLrel. 19, 1
                                                                                                                                                                                                                            583 AA;
HGN-
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                                                                                                                                                          Conservative
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                                                                                                                                                                                                                            66156 MW;
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 -TNEDSGCILPSTS-
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                                                                                                                                                            Score 764.5; 1
Pred. No. 1.6e
56; Mismatches
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annotation
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Query Match
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Matches 210; Conser
                                                                                                                                                                                                                  InterPro: IPRO00536; Hormone_rec
InterPro: IPRO01723; Strdhormone
InterPro: IPRO01628; zf-C4.
Pfam: PF00104; hormone_rec; 1.
Pfam: PF00105; zf-C4; 1.
PFRNTS: PR00398; STRDHORMONER.
PRINTS: PR00398; STRDHORMONER.
PRINTS: PR00047: STRDIDFINGER.
SMART: SM00399; NDLI; 1.
SMART: SM00399; NDLI; 1.
PROSITE; PS00031; NUCLEAR_RECEPTONA-binding; Nuclear protein; Recepton in the processor of the processor
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Q9IBD5;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. EMBL; AB032075; BAA89539.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anguilla japonica (Japanese e Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Anguillidae; Anguilla.
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                                                                                                                                                                     SEQUENCE
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Score 756.5; DB 13
Pred. No. 7.1e-43;
14; Mismatches 192;
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                                                                                                                   AR-BETA.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Onco
Takeo J., Yamashita
                                                                          SEQUENCE FROM N.A. MEDLINE=99150354; PubMed=10026186;
                                                                                                                                                                                                                               093245;
                                                                                                                                                                                                                                          093245
                                            receptors.";
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                                                                                                              NCBI_TaxID=8022
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Best Local Similarity
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pfam; pF0216; Androgen_recep; 1.

pfam; pF00104; hormone_rec; 1.

pfam; pF00105; zf-C4; 1.

priNTS; pR00047; STROIDFINGER.

SMART; SM00439; HOLI; 1.

SMART; SM0039; ZnF_C4; 1.

PROSTTE; PS00031; NUCLEAR RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P06536;
InterPro; IPRO
InterPro; IPRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Nuclear protein;
                                                                                                                                 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IPVGL-----GGVCDSPNIVFRGPFQNVFHN------VKATLPSNTTVTETLDFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSYSFMQNKHPWEMRQTNR-----
                                                                                                                                                                                                                                                                                                          KPEPDGAFS-----SSCLGGNSKINS-----DSSFSVPIKQESTKHSCSGTSFKGNPTVN
                                                                                                                                                                                                                                                                                                                                                                                              ENV-----SITEYKC----PSERNARPLQSDTRVKMFKS--SPANDLTEEVATME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSPIMCHEKSPSVCSP------LNMTSSVCSPAGINSVSSTTASFGSFPVHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD---SISFSRTLESDARRIHFAKSSTGNKTGFSSVNELDYPNANGYGSGRPG---
                       LKKIGQLKSPEEDLP--TQGPTDAIQCVSPQSGLTFHS---
                                                SKKLGKLKGIHEEQPQQQQPPPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISRAL
                                                                             SWKSHGDLSSRRSDG----YPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCH
                                                                                                                                                                                                                                                                                          QTDPDRISSHVIPAHVCETGETMEDKYADYLQQQYSVKIKYEAISNEPAGTSW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                          NNVTLRSSVSSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSVSLGLTMDLNEMNDLGPNYAPSSAND-----QSQGNYLFQVPLLNCS-----GAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241;
                                                                                              YGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARK
                                                                                                                                 DWLDVSYTDARFEGGRDHMFPMEFFFP-------PQRTCLICADEASGCH
                                                                                                                                                                                     NPYSA--GPDSGFICNPYEYERGG-GLVRRERPTSEQWYPGGMLGRMPYPNSPYLKNEVG
                                                                                                                                                                                                              -PSSAIVGVNSG--GQSFHYRIGAQGTISLSRSARDQSF-----QHLSSFPPVNTLVE
                                                                                                                                                                                                                                                                PFPFMDGSYFSFMDDKDYYSLSGILGPPVPGFDGNCEGSGFPVGIKQEPDDGSYYPEASI
 TPSPVMVLENIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLP
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IPR001628; zf-C4.
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                                                                                                                                                                                                                                       -GSQYN----
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27.3%;
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Pred.
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                             QLVFLN---
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Best Local Similarity 29.6
Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                pfam; PF02166; Androgen_recep; 1
pfam; PF00104; hormone_rec; 1.
pfam; PF00105; zf-C4; 1.
pfan; PF00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00339; ZnF_C4; 1.
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Q9GKL7;
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Song J.H., Fahrenkrug S.C., Rohrer G.A., Wise T.H., Ford "Porcine androgen receptor (AR) cDNA cloning: Expression associates with FSH secretion in boars.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metázoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig)
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                           DNA-binding; Nuclear protein;
Zinc-finger.
SEQUENCE 896 AA; 97094 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF202775; AAG37994.1; HSSP; P06536; 1GDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001103; Androgen_recep.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
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 452
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                                                                                                  VVPSPDTQEKGAQEVPFPKTEEVESAISNG-VTGQLNIVQYIKPEPDGA---FSSSCLGG
                                                                                                                               PAPPDEDDS---
                                                                                                                                                    SSPANINNSRCSVSSPSNTNNRSTLSSPAASTYGSICSPVNNAFSYTASGTSAGSSTLRD 357
                                                                                                                                                                            SPQVQSRGPTGYLALDEK-----QQPSQQQSAPECHPESGCTPEPGAASAASKGLQQQP 134
                           SSTI-SDSAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLTGPPSVRPTPCAPL
                                                    NSKINSDS----
                                                                           ILSEAGTMQLLQQQ----QQQQQQQEAVSEGNSSGRAR-----
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    -FMDG
                                                                                                                                                                                                                                               16.9%;
29.6%;
                                                   SFSVPIKQESTKHSCSGTSFKGN-
    SYFSF-
                                                                                                                                                                                                                                   86;
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Last sequence up
                                                                                                                                                                                                                                   Score 748.5;
Pred. No. 3.4e
B6; Mismatches
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                                                                                                                                                                                                                                                                                                                         Receptor;
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                                                                                                                                -AAPSTLSLLGP
                                                                                                                                                                                                                                               748.5;
No. 3.
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                                                                                                                                                                                                                                                            DB 6;
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                                                                                                                                                                                                                                     206;
                                                                                                                                ----TFPGLSSCSTDLKD
                                                                                                                                                                                                                                                                                                   CRC64;
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                                                                               -EATGAPISSKDSYLGG
                                                                                                                                                                                                                                                            Length
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Sus.
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in pituitary
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042274;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROGESTERONE RECEPTOR PROTEIN HOMOLOG (FRAGMENT).
                                                                                                                                                                                                              Suwattana D., Joerg H., Rieder S., Stranzinger G.;
"A crocodile sequence homologous to progesterone receptor.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
              NON_TER
                                                            PRINTS; PR00398; STRDHORMONER PRINTS; PR00047; STROIDFINGER SMART; SM00430; HOLI; 1. SMART; SM00399; ZDF_C4; 1.
                                                                                                                                                                                                                                                               TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                  Archosauria; Croc
NCBI_TaxID=68455;
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                          Crocodylus siamensis
                                                                                                            Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1.
                                                                                                                                    InterPro; IPR000536; Hormone_rec_liq.
InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR (BY :
                                  Zinc-finger.
                                                  DNA-binding; Nuclear
                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNE 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDDQWAVIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIEPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSRSARDQSFQH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISR----ALTPSPVMVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTRDHVLPIDYYFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYTRPPQGLAGQEGDLAIPDIWYPGGVVSRVPYPSPSCVKSEMGPWMESYSGPYGDMRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGDLASLHGGGAPGPGSGSPSATSSSSWHTLFTAEESQLYGPCGGGGGGGSAGEAGAVAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKSGALDDVAAYPSNDYYNFPLALAGPPPPPPPPPPHHARIKLENPLDYGSAWAAAAAQCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----MDD-----KDYYSLS-GILGPPVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AECKGSLLDDGPGKSNEETAEYSPFKAGYTKGLDSESLGCSSGGEAGGSGTLELPSALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GFDGNCEGSGFP----VGIKQEPDDGSYYPEASIPSSAIVG-VNSGGQSFHYRIGAQGTI
                                                                                                                                                                          P06536; 1GDC
                                                                                                                                                                                     AF030321; AAB81722.1;
 360 Z
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Crocodylidae;
 A,
                                                           ZnF_C4;
              360
 40975
                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GEASSATSPTEEPA--
 WW.
                                                                                                                                                                                                                                                                                                              Crocodylinae;
                                               Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PQKTCLICGDEASGCHYGALTCGSCKVFF
 8D5A339AB25905BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LSSFP-PVNTLVES----WKS----HGD--LS
                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                  HORMONE
                                                Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    837
                                                                                                                                                                                                                                                                                                              Crocodylus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QKLTVSHIEGYECQPIFLNVLE
                                                                                                                                                                                                  RECEPTORS
                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     803
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RESULT

OD 100

OD 100
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Вb
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Best Local Similarity
                                                                                                             Query Match
Best Local
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                          InterPro; IPR001723; Strdhormone
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
SMART; SM00430; HOLI; 1.
                                                                                                                                                                                                          Zinc-finger.
NON_TER
SEQUENCE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colombe L., Fostier A., Bury N., Pakdel F., Guiguen Y.;

"A mineralocorticoid-like receptor in the rainbow trout,
mykiss: Cloning and characterization of its steroid bind.

Steroids 65:319-328(2000).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii, Weopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, 01-DEC-2001 (Tremblrel. 19, MINERALOCORTICOID RECEPTOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9IAC6
                                                                                                                                                                                                                                                                         SMART; SM00399; ZnF_C4; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF209873; AAI
HSSP; P06536; 1GDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9IAC6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000536; Hormone_rec_lig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20264048; PubMed=10802282;
                                           627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           844 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 LVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 LQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVNTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVDKIRRKNCPACRLRKC
  ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                     FKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHE 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ŦJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNELLARVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKSLPGFRNLHIDDQITLIQYSWMSLMVFALGWRSYKHVSGQMLYFAPDLILNE--QRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQAGMVLGGRKFKKFNKVKVVRTLDVALQQSSGLPEESQALAQRLSF-
FKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRVRKCLQAGMNLGARKSKKPGKLKGVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              844
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                                                                                       Similarity 67...
46; Conservative
                                                                                                                                                                                                            359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                             , noll; 1.
; ZnF_C4; 1
                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF61206.1;
                                                                                                                                                                                                            40284 MW;
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                                                                                                             16.9%;
67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Strdhormone_receptor zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
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3; Mismatches
                                                                                                                Score 745.5; DB 1
Pred. No. 1.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 747;
Pred. No. 1
                                                                                                                                                                                                               E10983C5109C89A6 CRC64
                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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..2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                            36;
                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTORS FAMILY
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                                                                                          Indels
                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPNHDIQF
                                                                                                                                        359;
                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 222; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9GKN9
Q9GKN9;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor gene.";
Anim. Genet. 31:288-289(2000).
-i- SUBCELLULAR LOCATION; NUCLEAR (BY
-i- SIMILARITY: BELONGS TO THE NUCLEAR
EMBL; AF161717; AAG40566.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00047; STROIDFINGER. SMART; SM00430; HOLI; 1. SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trakooljul N., Ponsuksili S., Schellander K., Wimmers K.; "A highly polymorphic repetitive polypyrimidine/polypurine (CCTTT)n sequence in the 5' untranslated sequence of the porcine androgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=20539123; PubMed=11086548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANDROGEN RECEPTOR AR.
      218
                                             414
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SSTI-SDSAKELCKAVSVSMGLGVEALEHLSPGEQLRGGCMYAPLLTGPPSVRPTPCAPL
                                                 NSKINSDS-----
                                                                                                                                 VVPSPDTQEKGAQEVPFPKTEEVESAISNG-VTGQLNIVQYIKPEPDGA---FSSSCLGG
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                                                                                                                                                                                                                     SSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRD
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PF00104;
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IPR000536; Hormone_rec_lig
IPR001628; zf-C4.
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zf-C4; 1.
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hormone_rec; 1.
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                                             -SFSVPIKQESTKHSCSGTSFKGN---
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                                                                                        -QQQQQQEAVSEGNSSGRAR-----
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actyla; Suina; Suidae;
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01-JAN-1999
01-DEC-2001
EMBL;
         Kelley D.B., Kamenetz F.R., Kelley D.B., Badea T.C.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. SUBCELULIAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS EMBL; U67129; AAC97386.1; -.
                                                                                               SEQUENCE FROM N.A.

MEDLLINE=95324753; PubMed=7601302;

Fischer L.M., Catz D., Kelley D.B.;

"Androgen-directed development of the Xenopus laevis larynx: of androgen receptor expression and tissue differentiation.";

Dev. Biol. 170:115-126(1995).
                                                                                                                                                                                                         cell
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MEDLINE=93376782; PubMed=7690145;
Fischer L., Catz D., Kelley D.;
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                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                     laevis (African clawed frog)
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ae; Xenopus.
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Best Local Similarity
Q9UN21 PRELIMINARY;
Q9UN21;
01-MAY-2000 (TrEMBLrel. 13,
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pfam; PF00104; hormone_rec; 1.
pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
InterPro;
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                                                                                            612
                                                                                                                    806
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                                                     14
                                                                                        FFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIH
                                                                                                                                                                                                                                                                                                                SDG-----YPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTCGSCKV
                                                                                                                                                                                                                                                                                                                                                    MIG-----PMKTEMAPWMEGYPGAFGEMR
                                                                                                                                                                                                                                                                                                                                                                                                       YSELSGFAHCGATAGWHTLFEEGQSSGSFAEAGPYSYPRSHGPAGADGEFPSDAWYPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFKGNPTVNPFPFMDGS--YFSFMDDKDYYSLSGILGP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSVSS-
                                                                                                                                           EPVVVCAGHDNNQPDSFALLLSSLNELGERQLVHVVKWAKALPGFRNLHVSDQMTVIQYS
                                                                                                                                                       EPEIVYAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQYS
                                                                                                                                                                                                                     EEQPQQQQPPPPPPPPQSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENI
                                                                                                                                                                                                                                              FFKRAAEGKOKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKAQE
                                                                                                                                                                                                                                                                                                 LEGGRDHLLPIDYYFP-------PQKTCLICGDEASGCHYGALTCGSCKV
                                                                                                                                                                                                                                                                                                                                                                            IVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSFPPVNTLVESWKS--HGDLSSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYK-----PTAFMEESPGYPS----RDFYSFQMALAPHGRIKVENPMEYGGGAWGAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTGQLNIVQYIKPEP---DGAFSSSCLGGNSKINSDSSFSVPIKQESTKHSC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EALEHLSAG---AGEAQQRGDCMYAHPPDTHKCQVAEEDKSDTRDGPFRRSSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAFSYTASGTSAGSSTLRD----VVPSPDT-----QEKGAQEVPFPKTEEVESAISNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt PALGDCPTELKEILGEQSGRILESEETPAEKEGFSGPPEGISDSAKELCKAVSVSLGLSM}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PANI-----NNSRCSVSSPSNTNNRSTLSSP---AASTVGSICSPVN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEAPGTHRWSEASPQD-GTPLN-----PWVTHPPAPWREAQAEAAPQNPAGRTEGAQF
                                                                                                                                                                                              ELDGSSVQ------GEGSKELSPGMG-----IPQLEGYS--CQPIFLNVLEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001103; Androgen_recep.
IPR000536; Hormone_rec_lig
IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 AA; 86973 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SPEDGGGGGGSSSAGGSEEKEQPCTDLALPEPAGGYRHRAMELTPSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                               -----DGNCEGSGFPVGIKQEP-----DDGSYYPEASIPSSA
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    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 739; DB 13;
Pred. No. 1.3e-41;
9; Mismatches 204
                             PRT;
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Best Local Sim
Matches 229;
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InterPro; IPR000336; Hormone_rec_lig
InterPro; IPR001628; zf-C4.
Pfam; PF02166; Androgen_recep; 1.
Pfam; PF00104; hormone_rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STCOLIDINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-BREAST CARCINOMA;
Jin C.H., Urcan-Bisel M.S., Schrader W.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARIT
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE
EMBL: AP162704; AAD45921.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells.'
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521
                            563
                                                         461
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               HGD--LSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRPSKICLVCGDEASGCHYGVVTC
                                                                                                                                                                                                                                                                                                                                                                                                           GLPQQL-----PAPPDEDD-----SAAPSTL-SLLGP-----TFPGLSSCSADLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPNAENRGSRSHSPAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSV 297
YGDMRLETARDHVLPIDYYFP
                                                         AGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSPTCVKSEMGPWMDSYSGP
                                                                                   IGAQGTISLSRSARDQSFQH---
                                                                                                                YGDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPCGGGGGGGGGGGGGGGG
                                                                                                                                            YYPEASIPSSAIVGVNSG-----GQSFHY---
                                                                                                                                                                        YKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPPHPHARIKLENPLDYGSAWAAAAAQCR 400
                                                                                                                                                                                                                                CKGSLLDDSAGKSTEDTAEY--SPFKGGYTKGLEGESLGCSGSAAAGSSGTLELPSTLSL
                                                                                                                                                                                                                                                          ----FMDGSYFSFMDDKDYYSLSGILGPPVPGFDG---NCEGS-----
                                                                                                                                                                                                                                                                                        STISDNAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVRPTPCAPLAE
                                                                                                                                                                                                                                                                                                                     SKINSDS-----SFSVPIKQESTKHSCSGTSFKGN---
                                                                                                                                                                                                                                                                                                                                                  ILSEASTMQLLQQQ----QQEAVSEGSSSGRA-----REASGAPTSSKDNYLGGT
                                                                                                                                                                                                                                                                                                                                                                              VVPSPDTQEKGAQEVPFPKTEEVESAISNGVTGQLNIVQYIKPEPDGAFSSS---CLGGN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                      SSPANINNSRCSVSSPSNTNNRSTLSSPAASTVGSICSPVNNAFSYTASGTSAGSSTLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPQAHRRGPTGYL-----VLDEEQQP-SQPQSALECHPERGCVPEP-----GAAVAASK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P06536; 1GDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor sequences in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      906 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score (
30.1%; Pred. Native 76; Misr
                                                                                                                                                                                                   ----GFPVGIKQEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97884 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone_rec_lig
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19,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OA1FA8802B2EDDAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         729.5; DB 4;
No. 6.6e-41;
                                                                          LSSFP-PVNTLVES---
 PQKTCLICGDEASGCHYGALTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205;
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                                                                                                                                                                                                                                                                                                                     -----PTVNPFP-----
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                                                                                                                                                                                                     ---DDGS-----
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563
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Best Local Similarity
Matches 217; Conser
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InterPro; IPR000158; Hormone_rec_lig.
InterPro; IPR0001628; zf-c4.
InterPro; IPR001628; zf-c4.
Pfam; PF02166; Androgen_recep; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-c4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00339; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-TESTIS; PubMed=9918846; MEDLINE-99119319; PubMed=9918846; Todo T., Ikeuchi T., Kobayashi T., Nagahama Y.; Todo T., Ikeuchi T., Kobayashi T., Nagahama Y.; "Fish androgen receptor: cDNA cloning, steroid activation of transcription in transfected mammalian cells, and tissue mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Crau
Actinopterygii; Neopterygii; Teleo
Anguillidae; Anguilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9YGV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 254:378-383(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB023960; BAA75464.1; HSSP; P06536; 1GDC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9YGV9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQITLIQYSWMCLSSFALSWRSYKHTNSQFLYFAPDLVFNE
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                                                                                                        RETTSQSDTCAGES -- CSEHQAT -- -TISETARELCNAVSVSLGLNLDLNDMNDLSSNQI
                                                                                                                                    SSISSPPSHCSVKSPVSSPNNVTLRSSVSSPANINNSRCSVSSPSN--TNNRSTLSSPAA
                                                                                                                                                                                                                                            SSTTASFGSFPVHSPITQGTPLTCSPNAENRGSRSHSP----AHASNVGSPLSSPLSSMK 269
SSTESDTSQAIYLFESSPGYTGVGLNALVRDCKCQSAREGTSTQQYDRGAMFKINRVNDL
                                                 STVGSICSPVNNAFSYTASGTSAGSSTL-RDVV-----PSPDTQEKGA------QEV
                                                                                                                                                                                                              SDAEARPGIFS-ESSLDTGDEITCKLQSDNQGVRASGPLLPGSSGCNSGQKSSLACTSQQ
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                                                                                                                                                                                                                                                                                                                       16.4%; Score 727; DB 13;
31.9%; Pred. No. 8.9e-41;
tive 87; Mismatches 244
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Teleostei; Anguilliformes; Anguilloidei;
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                                                                                                             PPPPOSPEEGTTYIAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIVYAGYDSS
                                                                                                                                                                                          PFPKTEEVESAISN-----GVTGQLNIVQYIK-PEPDGAFSSSCLGGNSKINSDSSFS
            SYKHTNSQFLYFAPDLVFNE
                                              QPDSAASLLTSLNELGERQLVKVVKWAKGMPGFRSLYVDDQMTVIQHSWMAVMVFALGWR
                                                                     KPDTAENLLSTLNRLAGKQMIQVVKWAKVLPGFKNLPLEDQITLIQYSWMCLSSFALSWR
                                                                                            DGQGQGPAEAELSVSPKYDLGFHTQ-----SMFLN----TLEATEPEVVNAGHDYG
                                                                                                                                             LCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPP
                                                                                                                                                                                                                                            FEYAKRGVV----SREGYSLEH--GFP--NNLARTPYSGSLKNELGDRLSGPYPDVSYRY
                                                                                                                                                                                                                                                                    YRIGAQGTISLSRSARDQSFQHLSSFPPVNTLVE---SWKSHGDLSSRRSDGYPVLEY--
                                                                                                                                                                                                                                                                                           EKYNVQYDATIKSEDGKTTSEREWGFQYRYNESCSTPSAPPRHCAHQNRAGPYNQFFFNP
                                                                                                                                                                                                                                                                                                         EGSGFPVGIKQEPDDGS------YYPEASIPSSA---IVGVNSGG---QSFH--
                                                                                                                                                                                                                                                                                                                                           LPV---NASHYSQNVSVRVEPQSDFSPIL-----YKS-----
                                                                                                                                                                                                                                                                                                                                                                                          PLQPAPPRHTSISDAKWDMEAGLCAQMEHKDSEKCANMDGAHSTS-----VFSQFDQL
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